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(71) Applicant (*for all designated States except US*): **PHARMACIA & UPJOHN COMPANY [US/US]**; 301 Henrietta Street, Kalamazoo, MI 49007 (US).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **LOWERY, David, E.** [US/US]; 1207 Woodland Drive, Portage, MI 49024 (US). **FULLER, Troy, E.** [US/US]; 111 Dreamfield Drive, Battle Creek, MI 49014 (US). **KENNEDY, Michael, J.** [US/US]; 2364 Quincy Avenue, Portage, MI 49024 (US).

(74) Agent: **WILLIAMS, Joseph, A., Jr.**; Marshall, Gerstein & Borun, 6300 Sears Tower, 233 South Wacker Drive, Chicago, IL 60606 (US).

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(54) Title: ANTI-BACTERIAL VACCINE COMPOSITIONS

(57) Abstract: Gram negative bacterial virulence genes are identified, thereby allowing the identification of novel anti-bacterial agents that target these virulence genes and their products, and the provision of novel gram negative bacterial mutants useful in vaccines.

ANTI-BACTERIAL VACCINE COMPOSITIONS

This application is a continuation-in-part of U.S. Patent Application Serial No: 09/545,199, filed April 6, 2000, which claims benefit of U.S. Provisional Patent Application Serial Nos. 60/153,453, filed September 10, 1999 and 60/128,689, filed April 9, 1999.

FIELD OF THE INVENTION

The present invention relates generally to the identification of genes responsible for virulence of *Pasteurellaceae* bacteria, thereby allowing for production of novel attenuated mutant strains useful in vaccines and identification of new anti-bacterial agents that target the virulence genes and their products.

BACKGROUND OF THE INVENTION

The family *Pasteurellaceae* encompasses several significant pathogens that infect a wide variety of animals. In addition to *P. multocida*, prominent members of the family include *Pasteurella (Mannheimia) haemolytica*, *Actinobacillus pleuropneumoniae* and *Haemophilus somnus*. *P. multocida* is a gram-negative, nonmotile coccobacillus which is found in the normal flora of many wild and domestic animals and is known to cause disease in numerous animal species worldwide [Biberstein, In M. Kilian, W. Frederickson, and E. L. Biberstein (ed.), *Haemophilus, Pasteurella, and Actinobacillus*. Academic Press, London, p. 61-73 (1981)]. The disease manifestations following infection include septicemias, bronchopneumonias, rhinitis, and wound infections [Reviewed in Shewen, *et al.*, In C. L. Gyles and C. O. Thoen (ed.), Pathogenesis of Bacterial Infections in Animals. Iowa State University Press, Ames, p. 216-225 (1993), incorporated herein by reference].

Infection by *P. multocida* generally results from invasion during periods of stress, but transmission may also occur by aerosol or contact exposure, or via flea and tick vectors. In fowl, *P. multocida* infection gives rise to acute to peracute septicemia, particularly prevalent in domestic turkeys and wild waterfowl under stress conditions associated with overcrowding, laying, molting, or severe

climatic change. In cattle, a similar hemorrhagic septicemia follows infection and manifests conditions including high fever and depression, generally followed by quick death. Transmission is most likely through aerosol contact, but infection can also arise during periods of significant climatic change. In rabbits, infection gives rise to recurring purulent rhinitis, generally followed by conjunctivitis, otitis media, sinusitis, subcutaneous abscesses, and chronic bronchopneumonia. In severe infections, rabbit mortality arises from acute fibrinous bronchopneumonia, septicemia, or endotoxemia. Disease states normally arise during periods of stress. In pigs, common *P. multocida* disease states include atrophic rhinitis and bacterial pneumonia. Similar pneumonia conditions are also detected in dogs, cats, goats, and sheep. *P. multocida* is commonly detected in oral flora of many animals and is therefore a common contaminant in bite and scratch wounds.

P. multocida strains are normally designated by capsular serogroup and somatic serotype. Five capsular serogroups (A, B, D, E, and F) and 16 somatic serotypes are distinguished by expression of characteristic heat-stable antigens. Most strains are host specific and rarely infect more than one or two animals. The existence of different serotypes presents a problem for vaccination because traditional killed whole cell bacteria normally provide only serotype-specific protection. However, it has been demonstrated that natural infection with one serotype can lead to immunological protection against multiple serotypes [Shewen, *et al.*, *In C. L. Gyles and C. O. Thoen (Ed.), Pathogenesis of Bacterial Infections in Animals*. Iowa State University Press, Ames, p. 216-225 (1993)] and cross protection can also be stimulated by using inactivated bacteria grown *in vivo* [Rimler, *et al.*, *Am J Vet Res.* 42:2117-2121 (1981)]. One live spontaneous mutant *P. multocida* strain has been utilized as a vaccine and has been shown to stimulate a strong immune response [Davis, *Poultry Digest.* 20:430-434 (1987), Schlink, *et al.*, *Avian Dis.* 31(1):13-21 (1987)]. This attenuated strain, however, has been shown to revert to a virulent state or cause mortality if the vaccine recipient is stressed [Davis, *Poultry Digest.* 20:430-434 (1987), Schlink, *et al.*, *Avian Dis.* 31(1):13-21 (1987)].

Another member of the *Pasteurella* family, *A. pleuropneumoniae* exhibits strict host specificity for swine and is the causative agent of highly contagious porcine pleuropneumonia. Infection normally arises in intensive breeding conditions, and is believed to occur by a direct mode of transmission. The disease is often fatal and, as a result, leads to severe economic loss in the swine producing industry. *A. pleuropneumoniae* infection may be chronic or acute, and infection is characterized by a hemorrhagic, necrotic bronchopneumonia with accompanying fibrinous pleuritis. To date, bacterial virulence has been attributed to structural proteins, including serotype-specific capsular polysaccharides, lipopolysaccharides, and surface proteins, as well as extracellular cytolytic toxins. Despite purification and, in some instances cloning, of these virulence factors, the exact role of these virulence factors in *A. pleuropneumoniae* infection is poorly understood.

Twelve serotypes of *A. pleuropneumoniae* have been identified based on antigenic differences in capsular polysaccharides and production of extracellular toxins. Serotypes 1, 5, and 7 are most relevant to *A. pleuropneumoniae* infection in the United States, while serotypes 1, 2, 5, 7, and 9 are predominant in Europe. There are at least three significant extracellular toxins of *A. pleuropneumoniae* that are members of the haemolysin family and are referred to as RTX toxins. RTX toxins are produced by many Gram negative bacteria, including *E. coli*, *Proteus vulgarisa*, and *Pasteurella haemolytica*, and the proteins generally share structural and functional characteristics. Toxins from the various serotypes differ, however, in host specificity, target cells, and biological activities.

The major *A. pleuropneumoniae* RTX toxins include ApxI, ApxII, and ApxIII. ApxI and ApxII have haemolytic activity, with ApxI being more potent. ApxIII shows no haemolytic activity, but is cytotoxic for alveolar macrophages and neutrophils. Most *A. pleuropneumoniae* serotypes produce two of these three toxins. For example, serotypes 1, 5, 9, and 11 express ApxI and ApxII, and serotypes 2, 3, 4, 6, and 8 express ApxII and ApxIII. Serotype 10, however, produces only ApxI, and serotypes 7 and 12 express only ApxII. Those *A. pleuropneumoniae* serotypes that produce both ApxI and ApxII are the most virulent strains of the bacteria.

The Apx toxins were demonstrated to be virulence factors in murine models and swine infection using randomly mutated wild type bacteria [Tascon, *et al.*, *Mol. Microbiol.* 14:207-216 (1994)]. Other *A. pleuropneumoniae* mutants have also been generated with targeted mutagenesis to inactivate the gene encoding the AopA outer membrane virulence protein [Mulks and Buysee, *Gene* 165:61-66 (1995)].

At least eleven serotypes (1, 2, 5-9, 12-14 and 16) have been demonstrated within *Mannheimia* [*Pasteurella*] *haemolytica* [Angen, *et al.*, *Vet Microbiol* 65(4):283-90 (1999)], a *Pasteurellaceae* species which is responsible for serious outbreaks of acute pneumonia in neonatal, weaned, growing and adult lambs, calves, and goats [Ackermann, *et al.*, *Microbes Infect* 2(9):1079-88 (2000)]. Transportation, viral infections, overcrowding, and other stressful conditions predispose animals to *M. haemolytica* infection [Ackermann, *et al.*, *supra*.] The leukotoxin (Lkt) of *M. haemolytica* is believed to play a significant role in pathogenesis, causing cell lysis and apoptosis that lead to the lung pathology characteristic of bovine shipping fever [Highlander, *et al.*, *Infect Immun* 68(7):3916-22 (2000)] as well as lung injury in bovine pneumonic pasteurellosis [Jeyaseelan, *et al.*, *Microb Pathog* 30(2):59-69 (2001)]. Lkt is a pore-forming exotoxin that has the unique property of inducing cytolysis only in ruminant leukocytes and platelets [Jeyaseelan, *et al.*, (2001), *supra*.]. Cytolysis of many cell types is mediated by arachidonic acid (AA) and its generation by phospholipases is regulated by G-protein-coupled receptors [Jeyaseelan, *et al.*, (2001) *supra*.] Recent studies indicate that *M. haemolytica* Lkt binds to bovine CD18, the common subunit of all beta2 integrins [Jeyaseelan, *et al.*, *Infect Immun* 68(1):72-9 (2000)]. It has also been shown that LFA-1 is a Lkt receptor, Lkt binding to LFA-1 is not target cell specific, Lkt binding to bovine LFA-1 correlates with calcium elevation and cytolysis, and bovine LFA-1 expression correlates with the magnitude of Lkt-induced target cell cytolysis [Jeyaseelan, *et al.*, *Infect Immun* 68(1):72-9 (2000)].

In attempts to produce vaccine compositions, traditional killed whole cell bacteria have provided only serotype-specific protection [MacInnes and Smart, *supra*], however, it has been demonstrated that natural infection with a highly virulent

serotype can stimulate strong protective immunity against multiple serotypes [Nielsen, *Nord Vet Med.* 31:407-13 (1979), Nielsen, *Nord Vet Med.* 36:221-234 (1984), Nielsen, *Can J Vet Res.* 29:580-582 (1988), Nielsen, *ACTA Vet Scand.* 15:80-89 (1994)]. One defined live-attenuated vaccine strain producing an inactive form of the ApxII toxin has shown promise for cross protection in swine [Prideaux, *et al.*, *Infection & Immunity* 67:1962-1966 (1999)], while other undefined live-attenuated mutants have also shown promise [Inzana, *et al.*, *Infect Immun.* 61:1682-6, (1993), Paltineanu, *et al.*, *In International Pig Veterinary Society*, 1992, p. 214, Utrera, *et al.*, *In International Pig Veterinary Society*, 1992, p. 213].

Because of the problems associated with vaccine formulations comprising bacterial strains with undefined, spontaneous mutations, there exists a need in the art for rational construction of live attenuated bacterial strains for use in vaccines that will safely stimulate protective immunity against homologous and heterologous *Pasteurellaceae* serotypes. There further exists a need to identify attenuated bacterial strains and genes required for bacterial virulence, thereby facilitating development of methods to identify anti-bacterial agents.

SUMMARY OF THE INVENTION

In general, the present invention provides materials and methods for production and use of vaccine compositions comprising attenuated gram negative bacteria. In one aspect, vaccine compositions of the invention comprise attenuated species in the *Pasteurellaceae* family of bacteria, which is known in the art and described, in part, in Dewhirst, *et al.*, *J. Bacteriol.* 174:2002-2013 (1992), incorporated herein by reference in its entirety. Species in the family include, but are not limited to, *A. actinomycetemcomitans*, *A. capsulatus*, *A. equuli*, *A. lignieresii*, *A. pleuropneumoniae* (*H. pleuropneumoniae*), *A. seminis*, *A. suis* (*H. suis*), *A. ureae* (*p. ureae*), *A. capsulatus*, Bisgaard taxon 11, *H. aegyptius*, *H. aphrophilus*, *H. aphrophilus* (*H. parainfluenzae*), *H. ducreyi*, *H. haemoglobinophilus*, *H. haemolyticus*, *H. influenzae*, *H. paracuniculus*, *H. paragallinarum*, *H. parahaemolyticus*, *H. parainfluenzae*, (*H. paraphrophilus*), *H.*

paraphrohaemolyticus, *H. paraphrophilus*, *H. parasuis*, *H. parasuis* type 5, *H. segnis*, *H. somnus*, *Haemophilus* minor group, *Haemophilus* taxon C, *P. aerogenes*, *P. anatis*, *P. avium* (*H. avium*), *P. canis*, *P. dagmatis*, *P. gallinarum*, *P. (Mannheimia) haemolytica*, *P. trehalosi* (*P. haemolytica* biotype T), *P. langaa*, *P. multocida*, *P. pneumotropica*, *P. stomatis*, *P. volantium* (*H. parainfluenzae*), *P. volantium*, *Pasteurella* species A, *Pasteurella* species B, and *Haemophilus paraphrohaemolyticus*. Preferably, vaccine compositions comprise attenuated *Pasteurella (Mannheimia) haemolytica*, *Actinobacillus pleuropneumoniae*, *Haemophilus somnus*, or *Pasteurella multocida* bacteria. In a most preferred embodiment, vaccine compositions of the invention comprise attenuated *Pasteurella multocida* and *A. pleuropneumoniae* bacterial strains.

One aspect of the invention provides gram negative bacterial organisms containing a functional mutation in a gene sequence represented by any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, or species homologs thereof, wherein the mutation inhibits or abolishes expression and/or biological activity of an encoded gene product (*i.e.*, the polypeptide encoded by a gene); said functional mutation resulting in attenuated virulence of the bacterial strain. Functional mutations that modulate (*i.e.*, increase or decrease) expression and/or biological activity of a gene product include insertions or deletions in the protein coding region of the gene itself or in sequences responsible for, or involved in, control of gene expression. Deletion mutants include those wherein all or part of a specific gene sequence is deleted. Also contemplated are compositions, and preferably vaccine compositions, comprising mutated and attenuated gram negative bacterial organisms, optionally comprising a suitable adjuvant and/or a pharmaceutically acceptable diluent or carrier. In order for a modified strain to be effective in a vaccine formulation, the attenuation must be significant enough to

prevent the pathogen from evoking severe clinical symptoms, but also insignificant enough to allow limited replication and growth of the bacteria in the host.

The invention also provides polynucleotides encoding gene products that are required for virulence in gram negative bacteria. Polynucleotides of the invention include DNA, such as complementary DNA, genomic DNA including complementary or anti-sense DNA, and wholly or partially synthesized DNA; RNA, including sense and antisense strands; and peptide nucleic acids as described, for example in Corey, *TIBTECH* 15:224-229 (1997). Virulence gene polynucleotides of the invention include those set forth in SEQ ID NOs:1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, or species homologs thereof, polynucleotides encoding a virulence gene product encoded by a polynucleotide of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, or a species homolog thereof, and polynucleotide that hybridize, under moderately to highly stringent conditions, to the noncoding strand (or complement) of any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, or species homologs thereof. The invention therefore comprehends gene sequences from *Pasteurellaceae* set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, as well as related gene sequences from other

gram negative bacterial organisms, including naturally occurring (*i.e.*, species homologs) and artificially induced variants thereof. The invention also comprehends polynucleotides which encode polypeptides deduced from any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 164, 166, 168, 170, 172, and 174, and species homologs thereof. Knowledge of the sequence of a polynucleotide of the invention makes readily available every possible fragment of that polynucleotide. The invention therefore provides fragments of a polynucleotide of the invention.

The invention further embraces expression constructs comprising polynucleotides of the invention. Host cells transformed, transfected or electroporated with a polynucleotide of the invention are also contemplated. The invention provides methods to produce a polypeptide encoded by a polynucleotide of the invention comprising the steps of growing a host cell of the invention under conditions that permit, and preferably promote, expression of a gene product encoded by the polynucleotide, and isolating the gene product from the host cell or the medium of its growth.

Identification of polynucleotides of the invention makes available the encoded polypeptides. Polypeptides of the invention include full length and fragment, or truncated, proteins; variants thereof; fusion, or chimeric proteins; and analogs, including those wherein conservative amino acid substitutions have been introduced into wild-type polypeptides. Antibodies that specifically recognize polypeptides of the invention are also provided, and include monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, humanized antibodies, human antibodies, and complementary determining region (CDR)-grafted antibodies, as well as compounds that include CDR sequences which specifically recognize a polypeptide of the invention. The invention also provides anti-idiotype antibodies immunospecific for antibodies of the invention.

According to another aspect of the invention, methods are provided for identifying novel anti-bacterial agents that modulate the function of gram negative bacteria virulence genes or gene products. Methods of the invention include screening potential agents for the ability to interfere with expression of virulence gene products encoded by the DNA sequences set forth in any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, or species homologs thereof, or screening potential agents for the ability to interfere with biological function of a bacterial gene product encoded in whole or in part by a DNA sequence set forth in any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, species homologs thereof, or the complementary strand thereof, followed by identifying agents that provide positive results in such screening assays. In particular, agents that interfere with the expression of virulence gene products include anti-sense polynucleotides and ribozymes that are complementary to the virulence gene sequences. The invention further embraces methods to modulate transcription of gene products of the invention through use of oligonucleotide-directed triplet helix formation.

Agents that interfere with the function of virulence gene products include variants of virulence gene products, binding partners of the virulence gene products and variants of such binding partners, and enzyme inhibitors (where the product is an enzyme).

Novel anti-bacterial agents identified by the methods described herein are provided, as well as methods for treating a subject suffering from infection with gram negative bacteria involving administration of such novel anti-bacterial agents in an amount effective to reduce bacterial presence.

Numerous additional aspects and advantages of the invention will become apparent to those skilled in the art upon consideration of the following detailed description of the invention which describes presently prepared embodiments thereof.

5

DETAILED DESCRIPTION OF THE INVENTION

"Virulence genes," as used herein, are genes whose function or products are required for successful establishment and/or maintenance of bacterial infection in a host animal. Thus, virulence genes and/or the proteins encoded thereby 10 are involved in pathogenesis in the host organism, but may not be necessary for growth.

"Signature-tagged mutagenesis (STM)," as used herein, is a method generally described in International Patent Publication No. WO 96/17951, incorporated herein by reference, and includes, for example, a method for identifying 15 bacterial genes required for virulence in a murine model of bacteremia. In this method, bacterial strains that each have a random mutation in the genome are produced using transposon integration; each insertional mutation carries a different DNA signature tag which allows mutants to be differentiated from each other. The tags comprise 40 bp variable central regions flanked by invariant "arms" of 20 bp 20 which allow the central portions to be co-amplified by polymerase chain reaction (PCR). Tagged mutant strains are assembled in microtiter dishes, then combined to form the "inoculum pool" for infection studies. At an appropriate time after inoculation, bacteria are isolated from the animal and pooled to form the "recovered pool." The tags in the recovered pool and the tags in the inoculum pool are separately 25 amplified, labeled, and then used to probe filters arrayed with all of the different tags representing the mutants in the inoculum. Mutant strains with attenuated virulence are those which cannot be recovered from the infected animal, *i.e.*, strains with tags that give hybridization signals when probed with tags from the inoculum pool but not when probed with tags from the recovered pool. In a variation of this method, non- 30 radioactive detection methods such as chemiluminescence can be used

Signature-tagged mutagenesis allows a large number of insertional mutant strains to be screened simultaneously in a single animal for loss of virulence. Screening nineteen pools of mutant *P. multocida* strains resulted in the identification of more than 60 strains with reduced virulence, many of which were confirmed to be attenuated in virulence by subsequent determination of an approximate LD₅₀ for the individual mutants. Screening of *A. pleuropneumoniae* mutants resulted in identification of more than 100 strains having mutations in 35 different genes. Of these, mutations in 22 genes results in significantly attenuated *A. pleuropneumoniae* strains. The nucleotide sequence of the open reading frame disrupted by the transposon insertion was determined by sequencing both strands and an encoded amino acid sequence was deduced. Novelty of both the polynucleotide and amino acid sequences was determined by comparison of the sequences with DNA and protein database sequences. Knowledge of the virulence genes in these species permitted identification of species homologs in *P. (Mannheimia) haemolytica*.

The identification of bacterial, and more particularly *P. multocida* *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* virulence genes provides for microorganisms exhibiting reduced virulence (i.e., attenuated strains), which are useful in vaccines. Such microorganisms include *Pasteurellaceae* mutants containing at least one functional mutation inactivating a gene represented by any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174. The worker of ordinary skill in the art will realize that a "functional mutation" may occur in protein coding regions of a gene of the invention, as well as in regulatory regions that modulate transcription of the virulence gene RNA.

The worker of ordinary skill will also appreciate that attenuated *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* strains of the invention include those bearing more than one functional mutation. More than one mutation may result in additive or synergistic degrees of attenuation. Multiple

mutations can be prepared by design or may fortuitously arise from a deletion event originally intended to introduce a single mutation. An example of an attenuated strain with multiple deletions is a *Salmonella typhimurium* strain wherein the *cya* and *crp* genes are functionally deleted. This mutant *S. typhimurium* strain has shown promise as a live vaccine.

Identification of virulence genes in *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* can provide information regarding similar genes in other pathogenic species. As an example, identification of the *aroA* gene led to identification of conserved genes in a diverse number of pathogens, including *Aeromonas hydrophila*, *Aeromonas salmonicida*, *Salmonella typhimurium*, *Salmonella enteritidis*, *Salmonella dublin*, *Salmonella gallanerum*, *Bordetella pertussis*, *Yersinia enterocolitica*, *Neisseria gonorrhoeae*, and *Bacillus anthracis*. In many of these species, attenuated bacterial strains bearing mutations in the *aroA* gene have proven to be effective in vaccine formulations. Using the virulence genes sequences identified in *P. multocida*, similar or homologous genes can be identified in other organisms, particularly within the *Pasteurella* family, as well as *A. pleuropneumoniae*, *P. (Mannheimia) haemolytica*, and *Haemophilus somnus*. Likewise, identification of *A. pleuropneumoniae* virulence genes can permit identification of related genes in other organisms. Southern hybridization using the *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* genes as probes can identify these related genes in chromosomal libraries derived from other organisms. Alternatively, PCR can be equally effective in gene identification across species boundaries. As still another alternative, complementation of, for example, a *P. multocida* mutant with a chromosomal library from other species can also be used to identify genes having the same or related virulence activity. Identification of related virulence genes can therefore lead to production of an attenuated strain of the other organism which can be useful as still another vaccine formulation. Examples of *P. multocida* genes that have been demonstrated to exist in other species (e.g. *P. (Mannheimia) haemolytica*, *A. pleuropneumoniae* and *H. somnus*) include genes *exbB*, *atpG*, *pnp*, *guaB* and *yigF*.

Attenuated *P. multocida* strains identified using STM are insertional mutants wherein a virulence gene has been rendered non-functional through insertion of transposon sequences in either the open reading frame or regulatory DNA sequences. These insertional mutants still contain all of the genetic information required for bacterial virulence and can possibly revert to a pathogenic state by deletion of the inserted transposon. Therefore, in preparing a vaccine formulation, it is desirable to take the information gleaned from the attenuated strain and create a deletion mutant strain wherein some, most, or all of the virulence gene sequence is removed, thereby precluding the possibility that the bacteria will revert to a virulent state.

The vaccine properties of an attenuated insertional mutant identified using STM are expected to be the same or similar to those of a bacteria bearing a deletion in the same gene. However, it is possible that an insertion mutation may exert "polar" effects on adjoining gene sequences, and as a result, the insertion mutant may possess characteristic distinct from a mutant strain with a deletion in the same gene sequence. Deletion mutants can be constructed using any of a number of techniques well known and routinely practiced in the art.

In one example, a strategy using counterselectable markers can be employed which has commonly been utilized to delete genes in many bacteria. For a review, see, for example, Reyrat, *et al.*, *Infection and Immunity* 66:4011-4017 (1998), incorporated herein by reference. In this technique, a double selection strategy is often employed wherein a plasmid is constructed encoding both a selectable and counterselectable marker, with flanking DNA sequences derived from both sides of the desired deletion. The selectable marker is used to select for bacteria in which the plasmid has integrated into the genome in the appropriate location and manner. The counterselectable marker is used to select for the very small percentage of bacteria that have spontaneously eliminated the integrated plasmid. A fraction of these bacteria will then contain only the desired deletion with no other foreign DNA present. The key to the use of this technique is the availability of a suitable counterselectable marker.

In another technique, the *cre-lox* system is used for site specific recombination of DNA. The system consists of 34 base pair *lox* sequences that are recognized by the bacterial *cre* recombinase gene. If the *lox* sites are present in the DNA in an appropriate orientation, DNA flanked by the *lox* sites will be excised by the *cre* recombinase, resulting in the deletion of all sequences except for one remaining copy of the *lox* sequence. Using standard recombination techniques, it is possible to delete the targeted gene of interest in the *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica* genome and to replace it with a selectable marker (e.g., a gene coding for kanamycin resistance) that is flanked by the *lox* sites. Transient expression (by electroporation of a suicide plasmid containing the *cre* gene under control of a promoter that functions in *P. multocida*, *A. pleuropneumoniae*, or *P. (Mannheimia) haemolytica*) of the *cre* recombinase should result in efficient elimination of the *lox* flanked marker. This process would result in a mutant containing the desired deletion mutation and one copy of the *lox* sequences.

In another approach, it is possible to directly replace a desired deleted sequence in the *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica* genome with a marker gene, such as green fluorescent protein (GFP), β -galactosidase, or luciferase. In this technique, DNA segments flanking a desired deletion are prepared by PCR and cloned into a suicide (non-replicating) vector for *P. multocida*, *A. pleuropneumoniae*, or *P. (Mannheimia) haemolytica*. An expression cassette, containing a promoter active in *P. multocida*, *A. pleuropneumoniae*, or *P. (Mannheimia) haemolytica* and the appropriate marker gene, is cloned between the flanking sequences. The plasmid is introduced into wild-type *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica*. Bacteria that incorporate and express the marker gene (probably at a very low frequency) are isolated and examined for the appropriate recombination event (i.e., replacement of the wild type gene with the marker gene).

The reduced virulence of these organisms and their immunogenicity may be confirmed by administration to a subject animal. While it is possible for an avirulent microorganism of the invention to be administered alone, one or more of

such mutant microorganisms are preferably administered in a vaccine composition containing suitable adjuvant(s) and pharmaceutically acceptable diluent(s) or carrier(s). The carrier(s) must be "acceptable" in the sense of being compatible with the avirulent microorganism of the invention and not deleterious to the subject to be immunized. Typically, the carriers will be water or saline which will be sterile and pyrogen free. The subject to be immunized is a subject needing protection from a disease caused by a virulent form of *P. multocida*, *A. pleuropneumoniae*, *P. (Mannheimia) haemolytica* or other pathogenic microorganisms.

It will be appreciated that the vaccine of the invention may be useful in the fields of human medicine and veterinary medicine. Thus, the subject to be immunized may be a human or other animal, for example, farm animals including cows, sheep, pigs, horses, goats and poultry (e.g., chickens, turkeys, ducks and geese) companion animals such as dogs and cats; exotic and/or zoo animals; and laboratory animals including mice, rats, rabbits, guinea pigs, and hamsters.

The invention also provides polypeptides and corresponding polynucleotides required for *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica* virulence. The invention includes both naturally occurring and non-naturally occurring polynucleotides and polypeptide products thereof. Naturally occurring virulence products include distinct gene and polypeptide species as well as corresponding species homologs expressed in organisms other than *P. multocida*, *A. pleuropneumoniae*, or *P. (Mannheimia) haemolytica* strains. Non-naturally occurring virulence products include variants of the naturally occurring products such as analogs and virulence products which include covalent modifications. In a preferred embodiment, the invention provides virulence polynucleotides comprising the sequences set forth in SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 and species homologs thereof, and polypeptides having amino acids sequences encoded by the polynucleotides.

The present invention provides novel purified and isolated *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* polynucleotides (e.g., DNA sequences and RNA transcripts, both sense and complementary antisense strands) encoding the bacterial virulence gene products. DNA sequences of the invention include genomic and cDNA sequences as well as wholly or partially chemically synthesized DNA sequences. Genomic DNA of the invention comprises the protein coding region for a polypeptide of the invention and includes variants that may be found in other bacterial strains of the same species. "Synthesized," as used herein and is understood in the art, refers to purely chemical, as opposed to enzymatic, methods for producing polynucleotides. "Wholly" synthesized DNA sequences are therefore produced entirely by chemical means, and "partially" synthesized DNAs embrace those wherein only portions of the resulting DNA were produced by chemical means. Preferred DNA sequences encoding *P. multocida* virulence gene products are set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, and species homologs thereof. Preferred *A. pleuropneumoniae* DNA sequences encoding virulence gene products are set out in SEQ ID NOs: 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, and species homologs thereof. Preferred *P. (Mannheimia) haemolytica* virulence gene products are set out in SEQ ID NOs: 166, 168, 170, 172 and 174, and species homologs thereof. The worker of skill in the art will readily appreciate that the preferred DNA of the invention comprises a double stranded molecule, for example, molecules having the sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 and species homologs thereof, along with the complementary molecule (the "non-coding strand" or "complement") having a sequence deducible from the sequence of SEQ ID NO: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53,

55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112,
114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144,
146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174,
according to Watson-Crick base pairing rules for DNA. Also preferred are
5 polynucleotides encoding the gene products encoded by any one of the
polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29,
31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102,
104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135,
136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166,
10 168, 170, 172, and 174 and species homologs thereof. The invention further embraces
species, preferably bacterial, homologs of the *P. multocida*, *A. pleuropneumoniae* and
P. (Mannheimia) haemolytica DNA.

The polynucleotide sequence information provided by the invention
makes possible the identification and isolation of polynucleotides encoding related
15 bacterial virulence molecules by well known techniques including Southern and/or
Northern hybridization, and polymerase chain reaction (PCR). Examples of related
polynucleotides include polynucleotides encoding polypeptides homologous to a
virulence gene product encoded by any one of the polynucleotides set out in SEQ ID
NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57,
20 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116,
118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148,
150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, and species
homologs thereof, and structurally related polypeptides sharing one or more biological
and/or physical properties of a virulence gene product of the invention.

25 The invention also embraces DNA sequences encoding bacterial gene
products which hybridize under moderately to highly stringent conditions to the
non-coding strand, or complement, of any one of the polynucleotides set out in SEQ
ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57,
58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116,
30 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146,

148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172 and 174, and
species homologs thereof. DNA sequences encoding virulence polypeptides which
would hybridize thereto but for the degeneracy of the genetic code are contemplated
by the invention. Exemplary high stringency conditions include a final wash in buffer
5 comprising 0.2X SSC/0.1% SDS, at 65°C to 75°C, while exemplary moderate
stringency conditions include a final wash in buffer comprising 2X SSC/0.1% SDS, at
35°C to 45°C. It is understood in the art that conditions of equivalent stringency can
be achieved through variation of temperature and buffer, or salt concentration as
described in Ausubel, *et al.* (Eds.), Protocols in Molecular Biology, John Wiley &
10 Sons (1994), pp. 6.0.3 to 6.4.10. Modifications in hybridization conditions can be
empirically determined or precisely calculated based on the length and the percentage
of guanosine/cytosine (GC) base pairing of the probe. The hybridization conditions
can be calculated as described in Sambrook, *et al.*, (Eds.), Molecular Cloning: A
15 Laboratory Manual, Cold Spring Harbor Laboratory Press: Cold Spring Harbor, New
York (1989), pp. 9.47 to 9.51.

Autonomously replicating recombinant expression constructions such
as plasmid and viral DNA vectors incorporating virulence gene sequences are also
provided. Expression constructs wherein virulence polypeptide-encoding
polynucleotides are operatively linked to an endogenous or exogenous expression
20 control DNA sequence and a transcription terminator are also provided. The
virulence genes may be cloned by PCR, using *P. multocida* genomic DNA as the
template. For ease of inserting the gene into expression vectors, PCR primers are
chosen so that the PCR-amplified gene has a restriction enzyme site at the 5' end
preceding the initiation codon ATG, and a restriction enzyme site at the 3' end after
25 the termination codon TAG, TGA or TAA. If desirable, the codons in the gene are
changed, without changing the amino acids, according to *E. coli* codon preference
described by Grosjean and Fiers, *Gene*, 18:199-209 (1982), and Konigsberg and
Godson, *Proc. Natl. Acad. Sci. (USA)*, 80:687-691 (1983). Optimization of codon
usage may lead to an increase in the expression of the gene product when produced in
30 *E. coli*. If the gene product is to be produced extracellularly, either in the periplasm of

E. coli or other bacteria, or into the cell culture medium, the gene is cloned without its initiation codon and placed into an expression vector behind a signal sequence.

According to another aspect of the invention, host cells are provided, including prokaryotic and eukaryotic cells, either stably or transiently transformed, 5 transfected, or electroporated with polynucleotide sequences of the invention in a manner which permits expression of virulence polypeptides of the invention. Expression systems of the invention include bacterial, yeast, fungal, viral, invertebrate, and mammalian cells systems. Host cells of the invention are a valuable 10 source of immunogen for development of antibodies specifically immunoreactive with the virulence gene product. Host cells of the invention are conspicuously useful in methods for large scale production of virulence polypeptides wherein the cells are grown in a suitable culture medium and the desired polypeptide products are isolated from the cells or from the medium in which the cells are grown by, for example, immunoaffinity purification or any of the multitude of purification techniques well 15 known and routinely practiced in the art. Any suitable host cell may be used for expression of the gene product, such as *E. coli*, other bacteria, including *P. multocida*, *Bacillus* and *S. aureus*, yeast, including *Pichia pastoris* and *Saccharomyces cerevisiae*, insect cells, or mammalian cells, including CHO cells, utilizing suitable 20 vectors known in the art. Proteins may be produced directly or fused to a peptide or polypeptide, and either intracellularly or extracellularly by secretion into the periplasmic space of a bacterial cell or into the cell culture medium. Secretion of a protein requires a signal peptide (also known as pre-sequence); a number of signal 25 sequences from prokaryotes and eukaryotes are known to function for the secretion of recombinant proteins. During the protein secretion process, the signal peptide is removed by signal peptidase to yield the mature protein.

To simplify the protein purification process, a purification tag may be added either at the 5' or 3' end of the gene coding sequence. Commonly used purification tags include a stretch of six histidine residues (U.S. Patent Nos. 5,284,933 and 5,310,663), a streptavidin-affinity tag described by Schmidt and Skerra, *Protein Engineering*, 6:109-122 (1993), a FLAG peptide [Hopp *et al.*, *Biotechnology*, 6:1205- 30

1210 (1988)], glutathione S-transferase [Smith and Johnson, *Gene*, 67:31-40 (1988)], and thioredoxin [LaVallie *et al.*, *Bio/Technology*, 11:187-193 (1993)]. To remove these peptide or polypeptides, a proteolytic cleavage recognition site may be inserted at the fusion junction. Commonly used proteases are factor Xa, thrombin, and enterokinase.

The invention also provides purified and isolated *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* virulence polypeptides encoded by a polynucleotide of the invention. Presently preferred are polypeptides comprising the amino acid sequences encoded by any one of the polynucleotides set out in SEQ ID NOs : 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 164, 166, 168, 170, 172 and 174, and species homologs thereof. The invention embraces virulence polypeptides encoded by a DNA selected from the group consisting of : a) the DNA sequence set out in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 164, 166, 168, 170, 172, and 174 and species homologs thereof; b) DNA molecules encoding *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica*. polypeptides encoded by any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 164, 166, 168, 170, 172, and 174, and species homologs thereof; and c) a DNA molecule, encoding a virulence gene product, that hybridizes under moderately stringent conditions to the DNA of (a) or (b).

The invention also embraces polypeptides that have at least about 99%, at least about 95%, at least about 90%, at least about 85%, at least about 80%, at least about 75%, at least about 70%, at least about 65%, at least about 60%, at least

about 55%, and at least about 50% identity and/or homology to the preferred polypeptides of the invention. Percent amino acid sequence "identity" with respect to the preferred polypeptides of the invention is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the residues in the virulence gene product sequence after aligning both sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Percent sequence "homology" with respect to the preferred polypeptides of the invention is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the residues in one of the virulence polypeptide sequences after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and also considering any conservative substitutions as part of the sequence identity. Conservative substitutions can be defined as set out in Tables A and B.

15

Table A
Conservative Substitutions I

	SIDE CHAIN CHARACTERISTIC		AMINO ACID
20	Aliphatic	Non-polar	G A P I L V
		Polar - uncharged	C S T M N Q
		Polar - charged	D E K R
25	Aromatic		H F W Y
	Other		N Q D E

Polypeptides of the invention may be isolated from natural bacterial cell sources or may be chemically synthesized, but are preferably produced by recombinant procedures involving host cells of the invention. Virulence gene products of the invention may be full length polypeptides, biologically active fragments, or variants thereof which retain specific biological or immunological activity. Variants may comprise virulence polypeptide analogs wherein one or more

of the specified (*i.e.*, naturally encoded) amino acids is deleted or replaced or wherein one or more non-specified amino acids are added: (1) without loss of one or more of the biological activities or immunological characteristics specific for the virulence gene product; or (2) with specific disablement of a particular biological activity of the virulence gene product. Deletion variants contemplated also include fragments lacking portions of the polypeptide not essential for biological activity, and insertion variants include fusion polypeptides in which the wild-type polypeptide or fragment thereof have been fused to another polypeptide.

Variant virulence polypeptides include those wherein conservative substitutions have been introduced by modification of polynucleotides encoding polypeptides of the invention. Conservative substitutions are recognized in the art to classify amino acids according to their related physical properties and can be defined as set out in Table A (from WO 97/09433, page 10, published March 13, 1997 (PCT/GB96/02197, filed 9/6/96). Alternatively, conservative amino acids can be grouped as defined in Lehninger, [Biochemistry], Second Edition; Worth Publishers, Inc. NY:NY (1975), pp.71-77] as set out in Table B.

**Table B
Conservative Substitutions II**

	<u>SIDE CHAIN CHARACTERISTIC</u>	<u>AMINO ACID</u>
	Non-polar (hydrophobic)	
25	A. Aliphatic:	A L I V P
	B. Aromatic:	F W
	C. Sulfur-containing:	M
	D. Borderline:	G
	Uncharged-polar	
30	A. Hydroxyl:	S T Y
	B. Amides:	N Q
	C. Sulfhydryl:	C
	D. Borderline:	G
	Positively Charged (Basic):	K R H
35	Negatively Charged (Acidic):	DE

Variant virulence products of the invention include mature virulence gene products, *i.e.*, wherein leader or signal sequences are removed, having additional amino terminal residues. Virulence gene products having an additional methionine residue at position -1 are contemplated, as are virulence products having additional methionine and lysine residues at positions -2 and -1. Variants of these types are particularly useful for recombinant protein production in bacterial cell types. Variants of the invention also include gene products wherein amino terminal sequences derived from other proteins have been introduced, as well as variants comprising amino terminal sequences that are not found in naturally occurring proteins.

10 The invention also embraces variant polypeptides having additional amino acid residues which result from use of specific expression systems. For example, use of commercially available vectors that express a desired polypeptide as a fusion protein with glutathione-S-transferase (GST) provide the desired polypeptide having an additional glycine residue at position -1 following cleavage of the GST component from the desired polypeptide. Variants which result from expression using other vector systems are also contemplated.

15 Also comprehended by the present invention are antibodies (*e.g.*, monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, humanized, human, and CDR-grafted antibodies, including compounds which include CDR sequences which specifically recognize a polypeptide of the invention) and other binding proteins specific for virulence gene products or fragments thereof. The term “specific for” indicates that the variable regions of the antibodies of the invention recognize and bind a virulence polypeptide exclusively (*i.e.*, are able to distinguish a single virulence polypeptides from related virulence polypeptides despite sequence identity, homology, or similarity found in the family of polypeptides), but may also interact with other proteins (for example, *S. aureus* protein A or other antibodies in ELISA techniques) through interactions with sequences outside the variable region of the antibodies, and in particular, in the constant region of the molecule. Screening assays to determine binding specificity of an antibody of the invention are well known and routinely practiced in the art. For a comprehensive discussion of such assays, see

Harlow *et al.* (Eds), Antibodies A Laboratory Manual; Cold Spring Harbor Laboratory; Cold Spring Harbor , NY (1988), Chapter 6. Antibodies that recognize and bind fragments of the virulence polypeptides of the invention are also contemplated, provided that the antibodies are first and foremost specific for, as defined above, a virulence polypeptide of the invention from which the fragment was derived.

The DNA and amino acid sequence information provided by the present invention also makes possible the systematic analysis of the structure and function of the virulence genes and their encoded gene products. Knowledge of a polynucleotide encoding a virulence gene product of the invention also makes available anti-sense polynucleotides which recognize and hybridize to polynucleotides encoding a virulence polypeptide of the invention. Full length and fragment anti-sense polynucleotides are provided. The worker of ordinary skill will appreciate that fragment anti-sense molecules of the invention include (i) those which specifically recognize and hybridize to a specific RNA (as determined by sequence comparison of DNA encoding a virulence polypeptide of the invention to DNA encoding other known molecules) as well as (ii) those which recognize and hybridize to RNA encoding variants of the family of virulence proteins. Antisense polynucleotides that hybridize to RNA encoding other members of the virulence family of proteins are also identifiable through sequence comparison to identify characteristic, or signature, sequences for the family of molecules.

The invention further contemplates methods to modulate gene expression through use of ribozymes. For a review, see Gibson and Shillitoe, *Mol. Biotech.* 7:125-137 (1997). Ribozyme technology can be utilized to inhibit translation of mRNA in a sequence specific manner through (i) the hybridization of a complementary RNA to a target mRNA and (ii) cleavage of the hybridized mRNA through nuclease activity inherent to the complementary strand. Ribozymes can be identified by empirical methods but more preferably are specifically designed based on accessible sites on the target mRNA [Bramlage, *et al.*, *Trends in Biotech* 16:434-438 (1998)]. Delivery of ribozymes to target cells can be accomplished using either

exogenous or endogenous delivery techniques well known and routinely practiced in the art. Exogenous delivery methods can include use of targeting liposomes or direct local injection. Endogenous methods include use of viral vectors and non-viral plasmids.

5 Ribozymes can specifically modulate expression of virulence genes when designed to be complementary to regions unique to a polynucleotide encoding a virulence gene product. "Specifically modulate" therefore is intended to mean that ribozymes of the invention recognizes only a single polynucleotide. Similarly, ribozymes can be designed to modulate expression of all or some of a family of proteins. 10 Ribozymes of this type are designed to recognize polynucleotide sequences conserved in all or some of the polynucleotides which encode the family of proteins.

The invention further embraces methods to modulate transcription of a virulence gene of the invention through use of oligonucleotide-directed triplet helix formation. For a review, see Lavrovsky, *et al.*, *Biochem. Mol. Med.* 62:11-22 (1997).

15 Triplet helix formation is accomplished using sequence specific oligonucleotides which hybridize to double stranded DNA in the major groove as defined in the Watson-Crick model. Hybridization of a sequence specific oligonucleotide can thereafter modulate activity of DNA-binding proteins, including, for example, transcription factors and polymerases. Preferred target sequences for hybridization 20 include transcriptional regulatory regions that modulate virulence gene product expression. Oligonucleotides which are capable of triplet helix formation are also useful for site-specific covalent modification of target DNA sequences. Oligonucleotides useful for covalent modification are coupled to various DNA damaging agents as described in Lavrovsky, *et al.* [*supra*].

25 The identification of *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* virulence genes renders the genes and gene products useful in methods for identifying anti-bacterial agents. Such methods include assaying potential agents for the ability to interfere with expression of virulence gene products represented by the DNA sequences set forth in any one of SEQ ID NOS: 1, 30 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68,

70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120,
122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152,
154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 and species homologs
thereof (*i.e.*, the genes represented by DNA sequences of SEQ ID NOS: 1, 3, 7, 9, 11,
5 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74,
76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124,
126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156,
158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 encode the virulence gene
product, or the DNA sequences of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23,
10 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84,
100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132,
134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163,
164, 166, 168, 170, 172, and 174 are adjacent the gene encoding the virulence gene
product, or are involved in regulation of expression of the virulence gene product), or
15 assaying potential agents for the ability to interfere with the function of a bacterial
gene product encoded in whole or in part by a DNA sequence set forth in any one of
SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53,
55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112,
114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144,
20 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174,
species homologs thereof, or the complementary strand thereof, followed by
identifying agents that are positive in such assays. Polynucleotides and polypeptides
useful in these assays include not only the genes and encoded polypeptides as
disclosed herein, but also variants thereof that have substantially the same activity as
25 the wild-type genes and polypeptides.

The virulence gene products produced by the methods described above
are used in high throughput assays to screen for inhibitory agents. The sources for
potential agents to be screened are chemical compound libraries, fermentation media
of *Streptomyces*, other bacteria and fungi, and cell extracts of plants and other
30 vegetations. For proteins with known enzymatic activity, assays are established based

on the activity, and a large number of potential agents are screened for ability to inhibit the activity. For proteins that interact with another protein or nucleic acid, binding assays are established to measure such interaction directly, and the potential agents are screened for ability to inhibit the binding interaction.

5 The use of different assays known in the art is contemplated according to this aspect of the invention. When the function of the virulence gene product is known or predicted by sequence similarity to a known gene product, potential inhibitors can be screened in enzymatic or other types of biological and/or biochemical assays keyed to the function and/or properties of the gene product. When
10 the virulence gene product is known or predicted by sequence similarity to a known gene product to interact with another protein or nucleic acid, inhibitors of the interaction can be screened directly in binding assays. The invention contemplates a multitude of assays to screen and identify inhibitors of binding by the virulence gene product. In one example, the virulence gene product is immobilized and interaction with a binding partner is assessed in the presence and absence of a putative inhibitor compound. In another example, interaction between the virulence gene product and its binding partner is assessed in a solution assay, both in the presence and absence of a putative inhibitor compound. In both assays, an inhibitor is identified as a compound that decreases binding between the virulence gene product and its binding
15 partner. Other assays are also contemplated in those instances wherein the virulence gene product binding partner is a protein. For example, variations of the di-hybrid assay are contemplated wherein an inhibitor of protein/protein interactions is identified by detection of a positive signal in a transformed or transfected host cell as described in PCT publication number WO 95/20652, published August 3, 1995.
20

25 Candidate inhibitors contemplated by the invention include compounds selected from libraries of potential inhibitors. There are a number of different libraries used for the identification of small molecule modulators, including: (1) chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules. Chemical
30 libraries consist of structural analogs of known compounds or compounds that are

identified as "hits" or "leads" via natural product screening. Natural product libraries are collections of microorganisms, animals, plants, or marine organisms which are used to create mixtures for screening by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of plants or marine organisms. Natural product libraries include polyketides, non-ribosomal peptides, and variants (non-naturally occurring) thereof. For a review, see *Science* 282:63-68 (1998). Combinatorial libraries are composed of large numbers of peptides, oligonucleotides, or organic compounds as a mixture. They are relatively easy to prepare by traditional automated synthesis methods, PCR, cloning, or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to modulate activity.

Still other candidate inhibitors contemplated by the invention can be designed and include soluble forms of binding partners, as well as binding partners as chimeric, or fusion, proteins. Binding partners as used herein broadly encompasses antibodies, antibody fragments, and modified compounds comprising antibody domains that are immunospecific for the expression product of the identified virulence gene.

Other assays may be used when a binding partner (*i.e.*, ligand) for the virulence gene product is not known, including assays that identify binding partners of the target protein through measuring direct binding of test binding partner to the target protein, and assays that identify binding partners of target proteins through affinity ultrafiltration with ion spray mass spectroscopy/HPLC methods or other physical and analytical methods. Alternatively, such binding interactions are evaluated indirectly using the yeast two-hybrid system described in Fields and Song, *Nature*, 340:245-246 (1989), and Fields and Sternglanz, *Trends in Genetics*, 10:286-292 (1994), both of

which are incorporated herein by reference. The two-hybrid system is a genetic assay for detecting interactions between two proteins or polypeptides. It can be used to identify proteins that bind to a known protein of interest, or to delineate domains or residues critical for an interaction. Variations on this methodology have been developed to clone genes that encode DNA-binding proteins, to identify peptides that bind to a protein, and to screen for drugs. The two-hybrid system exploits the ability of a pair of interacting proteins to bring a transcription activation domain into close proximity with a DNA-binding domain that binds to an upstream activation sequence (UAS) of a reporter gene, and is generally performed in yeast. The assay requires the construction of two hybrid genes encoding (1) a DNA-binding domain that is fused to a first protein and (2) an activation domain fused to a second protein. The DNA-binding domain targets the first hybrid protein to the UAS of the reporter gene; however, because most proteins lack an activation domain, this DNA-binding hybrid protein does not activate transcription of the reporter gene. The second hybrid protein, which contains the activation domain, cannot by itself activate expression of the reporter gene because it does not bind the UAS. However, when both hybrid proteins are present, the noncovalent interaction of the first and second proteins tethers the activation domain to the UAS, activating transcription of the reporter gene. When the virulence gene product (the first protein, for example) is already known to interact with another protein or nucleic acid, this assay can be used to detect agents that interfere with the binding interaction. Expression of the reporter gene is monitored as different test agents are added to the system; the presence of an inhibitory agent results in lack of a reporter signal.

When the function of the virulence gene product is unknown and no ligands are known to bind the gene product, the yeast two-hybrid assay can also be used to identify proteins that bind to the gene product. In an assay to identify proteins that bind to the first protein (the target protein), a large number of hybrid genes each encoding different second proteins are produced and screened in the assay. Typically, the second protein is encoded by a pool of plasmids in which total cDNA or genomic DNA is ligated to the activation domain. This system is applicable to a wide variety

of proteins, and it is not even necessary to know the identity or function of the second binding protein. The system is highly sensitive and can detect interactions not revealed by other methods; even transient interactions may trigger transcription to produce a stable mRNA that can be repeatedly translated to yield the reporter protein.

5 Other assays may be used to search for agents that bind to the target protein. One such screening method to identify direct binding of test ligands to a target protein is described in U.S. Patent No. 5,585,277, incorporated herein by reference. This method relies on the principle that proteins generally exist as a mixture of folded and unfolded states, and continually alternate between the two states. When a test ligand binds to the folded form of a target protein (i.e., when the test ligand is a ligand of the target protein), the target protein molecule bound by the ligand remains in its folded state. Thus, the folded target protein is present to a greater extent in the presence of a test ligand which binds the target protein, than in the absence of a ligand. Binding of the ligand to the target protein can be determined
10 by any method which distinguishes between the folded and unfolded states of the target protein. The function of the target protein need not be known in order for this assay to be performed. Virtually any agent can be assessed by this method as a test ligand, including, but not limited to, metals, polypeptides, proteins, lipids, polysaccharides, polynucleotides and small organic molecules.
15

20 Another method for identifying ligands for a target protein is described in Wieboldt *et al.*, *Anal. Chem.*, 69:1683-1691 (1997), incorporated herein by reference. This technique screens combinatorial libraries of 20-30 agents at a time in solution phase for binding to the target protein. Agents that bind to the target protein are separated from other library components by centrifugal ultrafiltration. The
25 specifically selected molecules that are retained on the filter are subsequently liberated from the target protein and analyzed by HPLC and pneumatically assisted electrospray (ion spray) ionization mass spectroscopy. This procedure selects library components with the greatest affinity for the target protein, and is particularly useful for small molecule libraries.

The inhibitors/binders identified by the initial screens are evaluated for their effect on virulence in *in vivo* mouse models of *P. multocida* infections. Models of bacteremia, endocarditis, septic arthritis, soft tissue abscess, or pneumonia may be utilized. Models involving use of other animals are also comprehended by the invention. For example, rabbits can be challenged with a wild type *P. multocida* strain before or after administration of varying amounts of a putative inhibitor/binder compound. Control animals, administered only saline instead of putative inhibitor/binder compound provide a standard by which deterioration of the test animal can be determined. Other animal models include those described in the Animal and Plant Health Inspection Service, USDA, January 1, 1994 Edition, §§113.69-113.70; Panciera and Corstvet, *Am. J. Vet. Res.* 45:2532-2537; Ames, *et al.*, *Can. J. Comp. Med.* 49:395-400 (1984); and Mukkur, *Infection and Immunity* 18:583-585 (1977). Inhibitors/binders that interfere with bacterial virulence are can prevent the establishment of an infection or reverse the outcome of an infection once it is established.

Any adjuvant known in the art may be used in the vaccine composition, including oil-based adjuvants such as Freund's Complete Adjuvant and Freund's Incomplete Adjuvant, mycolate-based adjuvants (*e.g.*, trehalose dimycolate), bacterial lipopolysaccharide (LPS), peptidoglycans (*i.e.*, mureins, mucopeptides, or glycoproteins such as N-Opaca, muramyl dipeptide [MDP], or MDP analogs), proteoglycans (*e.g.*, extracted from *Klebsiella pneumoniae*), streptococcal preparations (*e.g.*, OK432), Biostim™ (*e.g.*, 01K2), the "Iscoms" of EP 109 942, EP 180 564 and EP 231 039, aluminum hydroxide, saponin, DEAE-dextran, neutral oils (such as miglyol), vegetable oils (such as arachis oil), liposomes, Pluronic® polyols, the Ribi adjuvant system (see, for example GB-A-2 189 141), or interleukins, particularly those that stimulate cell mediated immunity. An alternative adjuvant consisting of extracts of *Amycolata*, a bacterial genus in the order Actinomycetales, has been described in U.S. Patent No. 4,877,612. Additionally, proprietary adjuvant mixtures are commercially available. The adjuvant used will depend, in part, on the

recipient organism. The amount of adjuvant to administer will depend on the type and size of animal. Optimal dosages may be readily determined by routine methods.

The vaccine compositions optionally may include vaccine-compatible pharmaceutically acceptable (*i.e.*, sterile and non-toxic) liquid, semisolid, or solid diluents that serve as pharmaceutical vehicles, excipients, or media. Any diluent known in the art may be used. Exemplary diluents include, but are not limited to, polyoxyethylene sorbitan monolaurate, magnesium stearate, methyl- and propylhydroxybenzoate, talc, alginates, starches, lactose, sucrose, dextrose, sorbitol, mannitol, gum acacia, calcium phosphate, mineral oil, cocoa butter, and oil of theobroma.

The vaccine compositions can be packaged in forms convenient for delivery. The compositions can be enclosed within a capsule, caplet, sachet, cachet, gelatin, paper, or other container. These delivery forms are preferred when compatible with entry of the immunogenic composition into the recipient organism and, particularly, when the immunogenic composition is being delivered in unit dose form. The dosage units can be packaged, *e.g.*, in tablets, capsules, suppositories or cachets.

The vaccine compositions may be introduced into the subject to be immunized by any conventional method including, *e.g.*, by intravenous, intradermal, intramuscular, intramammary, intraperitoneal, or subcutaneous injection; by oral, sublingual, nasal, anal, or vaginal, delivery. The treatment may consist of a single dose or a plurality of doses over a period of time.

The invention also comprehends use of an attenuated bacterial strain of the invention for manufacture of a vaccine medicament to prevent or alleviate bacterial infection and/or symptoms associated therewith. The invention also provides use of inhibitors of the invention for manufacture of a medicament to prevent or alleviate bacterial infection and/or symptoms associated therewith.

The present invention is illustrated by the following examples. Example 1 describes constructions of *P. multocida* mutants. Example 2 relates to screening for *P. multocida* mutants. Example 3 addresses methods to determine

virulence of the *P. multocida* mutants. Example 4 describes cloning of *P. multocida* virulence genes. Example 5 addresses identification of genes in other species related to *P. multocida* virulence genes. Example 6 describes construction of *A. pleuropneumoniae* mutants. Example 7 addresses screening for attenuated *A. pleuropneumoniae* mutants. Example 8 relates to identification of *A. pleuropneumoniae* virulence genes. Example 9 describes competition challenge of *A. pleuropneumoniae* mutants and wild type bacteria. Example 10 characterizes *A. pleuropneumoniae* genes identified. Example 11 addresses efficacy of *A. pleuropneumoniae* mutant to protect against wild type bacterial challenge. Example 12 describes identification of species homolog virulence genes in *P. (Mannheimia) haemolytica*.

Example 1

Construction of a Library of Tagged-Transposon *P. multocida* Mutants

A library of tagged-transposon mutants was constructed in parental vector pLOF/Km [Herrero, et al., *J Bacteriol.* 172:6557-67 (1990)] which has previously been demonstrated to be functional and random in *P. multocida* [Lee, et al., *Vet Microbiol.* 50:143-8 (1996)]. Plasmid pLOF/Km was constructed as a modification of suicide vector pGP704 and included a transposase gene under control of the *Tac* promoter as well as the mini-Tn10 transposable element encoding kanamycin resistance. Plasmid pTEF-1 was constructed as described below by modifying pLOF/Km to accept sequence tags which contained a semi-random [NK]₃₅ sequence.

Plasmid pLOF/Km was first modified to eliminate the unique *KpnI* restriction site in the multiple cloning region and then to introduce a new *KpnI* site in the mini-Tn10 region. The plasmid was digested with *KpnI* and the resulting overhanging ends were filled in with Klenow polymerase according to manufacturer's suggested protocol. Restriction digests and ligations described herein were performed according to manufacturer's suggested protocols (Gibco BRL, Gaithersburg, MD and Boehringer Mannheim, Indianapolis, IN). The blunt end product was self-ligated to

produce a plasmid designated pLOF/Km--*KpnI* which was transformed into *E.coli* DH5 α :: λ pir for amplification. *E.coli* DH5 α : (λ pir ϕ 80dlacZ Δ M15, recA1, endA1, gyrA96, thi-1, hsdR17(r_k, m_k, supE44, relA1, deoR, Δ (lacZYA-argF)U169, was propagated at 37°C in Luria-Bertani (LB) medium. Plasmids were prepared using
5 QIAGEN SpinPreps from QIAGEN Inc. (Santa Clarita, CA) and digested with *Sfi*I which cuts at a unique site within the mini-Tn10 transposable element. A *Sfi*I-*KpnI*-*Sfi*I adaptor was prepared by annealing oligonucleotides TEF1 (SEQ ID NO: 86) and TEF3 (SEQ ID NO: 87) and the resulting double-stranded adapter was ligated into the
10 *Sfi*I site to create plasmid pTEF-1. Oligonucleotides TEF1 and TEF3 (as well as all other oligonucleotides described herein) were synthesized by Genosys Biotechnologies (The Woodlands, TX).

TEF1 5'-AGGCCGGTACCGGCCGCCT SEQ ID NO: 86

15 TEF3 5'-CGGCCGGTACCGGCCTAGG SEQ ID NO: 87

Unique sequence tags for insertion into the *KpnI* site of pTEF-1 were prepared as follows. PCR was carried out to generate double stranded DNA tags using a GeneAmp XL PCR Kit (PE Applied Biosystems, Foster City, CA) under conditions including 250 μ M each dNTP, 1.5 mM Mg(OAc)₂, 100 pmol each primer
20 TEF14 (SEQ ID NO: 88) and TEF15 (SEQ ID NO: 89), 1 ng TEF26 (SEQ ID NO: 90) as template DNA and 2.5 units recombinant *Tth* DNA Polymerase XL.

TEF14 5'-CATGGTACCCATTCTAAC SEQ ID NO: 88

25

TEF15 5'-CTAGGTACCTACAACCTC SEQ ID NO: 89

TEF26 SEQ ID NO: 90

5'-CTAGGTACCTACAACCTCAAGCTT-[NK]₃₅-

30

AAGCTTGGTTAGAATGGGTACCATG

Reaction conditions included an initial incubation at 95°C for one minute, followed by thirty cycles of 30 seconds at 95°C, 45 seconds at 45°C, and 15 seconds at 72°C, followed by a final incubation at 72°C for two minutes. The PCR products were digested with *Kpn*I and purified using a QIAGEN Nucleotide Removal Kit (QIAGEN, Inc., Chatsworth, GA) according to the manufacturer's suggested protocol. The unique tag sequences were ligated into the mini-Tn10 element of linearized pTEF-1, previously digested with *Kpn*I and dephosphorylated with calf intestinal alkaline phosphatase (Boehringer Mannheim) using standard procedures. The resulting plasmid library was transformed into *E.coli* DH5 α : λ pir. Colony blot analysis was performed according to the DIG User's Guide (Boehringer-Mannheim) with hybridization and detection performed as follows.

Hybridizations were essentially performed according to the Genius Non-Radioactive User's Guide (Boehringer Mannheim Biochemicals), the product sheet for the DIG-PCR labeling kit (Boehringer Mannheim Biochemicals), and the product sheet for CSPD (Boehringer Mannheim Biochemicals). For preparation of probes, a 100 μ l primary PCR reaction was set up using Amplitaq PCR buffer (PE Applied Biosystems), 200 μ M dNTPs, 140 pmol each of primers TEF5 (SEQ ID NO: 91) and TEF6 (SEQ ID NO: 92), 2 mM MgCl₂, 2.5 units Amplitaq (PE Applied Biosystems) and 1 ng of plasmid DNA.

20

TEF5 5'-TACCTACAACCTCAAGCT SEQ ID NO: 91

TEF6 5'-TACCCATTCTAACCAAGC SEQ ID NO: 92

25 Cycle conditions included an initial incubation at 95°C for two minutes, followed by 35 cycles of 95°C for 30 seconds, 50°C for 45 seconds, 72°C for 15 seconds and a final incubation at 72°C for three minutes. The amplification products were separated using electrophoresis on a 2% - 3:1 NuSieve GTG (FMC BioProducts, Rockland, ME, USA):Agarose gel and the 109 bp product was excised and purified. Gel 30 extractions were carried out using a QIAGEN Gel Extraction kit (QIAGEN).

Approximately 15 ng of the primary product was labeled in a 50 µl PCR reaction using the DIG PCR Kit, 50 pmol each of primers TEF24 and TEF25, and a 1:1 mix of DIG Probe Synthesis Mix with 2 mM dNTP stock solution.

5 TEF24 5'-TACCTACAACCTCAAGCTT SEQ ID NO: 93

TEF25 5'-TACCCATTCTAACCAAGCTT SEQ ID NO: 94

PCR conditions included an initial incubation at 95°C for four minutes, followed by
10 25 cycles of 95°C for 30 seconds, 50°C for 45 seconds, 72°C for 15 seconds and a final incubation at 72°C for three minutes. The labeled PCR product was digested with *Hind*III in a total reaction volume of 90 µl and purified from the constant primer arms using a 2% - 3:1 NuSieve GTG (FMC BioProducts):Agarose gel. The region containing the labeled variable tag was excised and the entire gel slice was dissolved
15 and denatured in 10 ml of DIG EasyHyb at 95°C for ten minutes.

Dot blots were prepared using a Hybond[®]-N⁺ membrane (Amersham-
Pharmacia Biotech). Target DNA for each tag was prepared in 96 well plates using approximately 30 ng of PCR product. An equal volume of 0.1 N NaOH was added to denature the sample and each sample was applied to the membrane with minimal
20 vacuum using a Minifold ITM Dot-Blot Apparatus from Schleicher and Schuell (Keene, NH, USA). Each well was washed with 150 µl of Neutralization Solution (0.5 M Tris /3 M NaCl, pH 7.5) and 150 µl of 2X SSC. Membranes were UV-crosslinked in a Stratalinker (Stratagene, La Jolla, CA, USA) and prehybridized for one hour in 20 mls DIG EasyHyb Buffer at 42°C. The denatured probe was added and
25 hybridization carried out overnight at 42°C. The membrane was washed two times in 2X SSC containing 0.1% SDS for five minutes each wash. Two high stringency washes were performed in 50 ml of pre-warmed 0.1X SSC buffer containing 0.1% SDS at 68°C for 15 minutes before proceeding with standard Genius Detection protocols (Genius Manual).

It is desirable to use a non-radioactive detection system for safety, lower cost, ease of use, and reduction of hazardous materials. In initial experiments using similar procedures previously described [Mei, *et al.*, *Mol Microbiol.* 26:399-407 (1997)], unacceptable background levels of hybridization were obtained in negative controls. In order to decrease background, tag length was increased by 30 bp to a total of 70, amplification primers were lengthened to include all sequence flanking the variable region, a lower concentration of dig-dUTP was used, and the conserved sequences flanking the sequence tag region were removed by gel purification. Most significantly, PCR was used to generate [NK]₃₅ sequence tags as the target DNA in dot blots rather than the entire plasmids containing the tagged transposons after detecting background hybridization from the transposon itself. Using these modifications background was eliminated making chemiluminescent/non-radioactive screening more effective.

Approximately four hundred different transformants resulting from the ligation of pTEF-1 with the PCR generated sequence tags were screened by colony blot and the 96 strongest hybridizing colonies were assembled into microtiter plates for further use. Even though the likelihood of duplicated tags was very low, half of the plate of master tags was probed against the other to confirm that no tags were duplicated. The plasmids containing these tags were purified and transformed into *E.coli* S17-1:λpir (*pir, recA, thi, pro, hsd, (r-m+)*), RP4-2, (Tc::Mu), (Km::Tn7), [TmpR], [SmR]), and the transformed bacteria propagated at 37°C in Luria-Bertani (LB) medium. Each of the 96 *E.coli* S17-1:λpir transformants containing the tagged plasmid pTEF-1 was used in conjugative matings to generate transposon mutants of *P. multocida*. *P. multocida* strain TF5 is a spontaneous nalidixic acid resistant mutant derived from UC6731, a bovine clinical isolate. *P. multocida* strains were grown on brain heart infusion (BHI) media (Disco Laboratories, Detroit, MI, USA) at 37°C and in 5% CO₂ when grown on plates. Matings were set up by growing each *E.coli* S17-1:λpir /pTEF1:[NK]₃₅ clone and the TF5 strain to late log phase. Fifty μl of culture for each tagged-pTEF-1 clone was mixed with 200 μl of the TF5 culture and 50 μl of each mating mixture was spotted onto 0.22 TM filters previously placed on BHI plates

containing 100 mM IPTG and 10 mM MgSO₄. Following overnight incubation at 37°C with 5% CO₂, mating mixtures were washed off of each filter into 3 ml of PBS and 25 µl of each was plated onto BHIN⁵⁰K¹⁰⁰ plates. Following selective overnight growth, colonies were assembled into microtiter plates by toothpick transfer into 200 5 µl BHIN⁵⁰K⁵⁰ making sure that each well in a microtiter plate always contained a transposon mutant with the same sequence tag. Following overnight growth, 50 µl of 75% glycerol was added to each well and plates were stored frozen at -80°C.

10 Nineteen pools were assembled by transferring the transposon mutants to microtiter plates making sure that each well contained a transposon mutant with the appropriate tag for that well. In other words, a specific well in each microtiter plate always contained a transposon mutant with the same sequence tag even though the location of the transposon within those mutants may be different.

15 **Example 2**
Murine Screening for Attenuated *P. multocida* Mutants

Nineteen pools of *Pasteurella multocida* transposon mutants were screened using a murine model of septicemia. Frozen plates of pooled *P. multocida* transposon mutants were removed from -80°C storage and subcultured by transferring 10 µl from each well to a new 96 well round bottom plate (Corning Costar, 20 Cambridge, MA, USA) containing 200 µl of brain heart infusion (DIFCO) with 50 µg/ml nalidixic acid (Sigma) and 50 µg/ml kanamycin (Sigma) (BHIN⁵⁰K⁵⁰). Plates were incubated without shaking overnight at 37°C in 5% CO₂. Overnight plates were subcultured by transferring 10 µl from each well to a new flat bottomed 96-well plate (Corning Costar) containing 100 µl of BHI per well and incubating at 37°C with 25 shaking at approximately 150 rpm. The OD₅₄₀ was monitored using a micro-titer plate reader. At an OD₅₄₀ of approximately 0.2 to 0.25, each plate was pooled to form the “input pool” by combining 100 µl from each of the wells of the micro-titer plate. The culture was diluted appropriately in BHI to doses of approximately 10⁴, 10⁵, 10⁶ CFU/ml and 0.2 ml of each dilution was used to infect female 14-16 g BALB/c mice 30 by intraperitoneal administration. At two days post-infection, one or two surviving mice were euthanized and the spleens harvested. The entire spleen was homogenized

in 1.0 ml sterile 0.9 % saline. Dilutions of the homogenate from 10^{-2} to 10^{-5} were prepared and plated onto BHIN⁵⁰K⁵⁰ plates. Following overnight growth, at least 20,000 colonies were pooled in 10 mls BHI broth to form the "recovered pool" and 0.5 ml of the recovered pool was centrifuged at 3,500 X g and the pellet used to 5 prepare genomic DNA according to a previously described protocol [Wilson, *In F. M. Ausubel, et al., (ed.), Current Protocols in Molecular Biology*, vol. 1. John Wiley and Sons, New York, p. 2.4.1-2.4.5. (1997)].

Initial experiments with virulent wild-type *P. multocida* indicated that 10 organisms could be recovered from the spleen, lungs, kidneys, and liver indicating a truly septicemic model of infection. Dot blots for both the "input" and "recovered" pools were performed as described in Example 1 and evaluated both by visual inspection and by semi-quantitative analysis. Hybridization was carried out as described in Example 1 except that 5 µg of genomic DNA from input and recovered pools was used as template. Semi-quantitative analysis indicates whether a significant 15 reduction in a single clone has occurred. If a mutant is unable to survive within the host, then the recovered signal should be very low compared to the input signal yielding a high input/recovered ratio. Most mutants will grow as well *in vivo* as *in vitro* and therefore a ratio of their signals should be approximately equal to 1. Clones selected by quantitative analysis as being highly reduced in the recovered pool were 20 selected for further study. Additional clones with questionable input/recovered ratios were also selected after visually evaluating films made from the dot blots.

Example 3 Determination of Virulence for *P. multocida* Candidate Mutants

Each potential mutant which exhibited reduced recovery from splenic 25 tissue was isolated from the original pool plate and used individually in a challenge experiment to verify and roughly estimate the attenuation caused by the transposon mutation. Individual candidate mutants from *in vivo* screens were grown on Sheep Blood Agar plates overnight in 5% CO₂ at 37°C. Approximately six colonies of each 30 mutant were inoculated into BHI broth and allowed to grow for six hours. Dilutions were prepared and five mice each were infected as described above with 10^2 , 10^3 , 10^4

and 10^5 CFU each. Attenuation was determined by comparing mortality after six days relative to the wild type. Surviving mice were presumed to be protected and then challenged with a dose of wild type *P. multocida* at a concentration approximately 200-fold greater than the LD₅₀ for the wild type strain. Survival rate was then determined for each challenged group of mice.

Results indicated that 62 of 120 potential transposon mutants were attenuated, having an approximate LD₅₀ of at least 10 fold higher than the wild type strain. The clones and their approximate LD₅₀ values are listed in Table 1. A control experiment with the wild type strain was run in parallel with each set of challenges and in all cases mortality in wild type-challenged groups was 100%.

In addition to LD₅₀ values, Table 1 also provides data from vaccination and challenge experiments. Briefly, groups of mice (n = 5 to 10) were vaccinated by intraperitoneal injection with the individual *P. multocida* strains shown in Table 1 at a dose that was approximately 200 times greater than the LD₅₀ of the virulent, wild type strain. Animals were observed for 28 days after which mortality figures were calculated.

Table 1
P. multocida Virulence Genes

Nucleotide SEQ ID NO:	Representative Isolate	PossibleGene Function	Vaccination # survivors/total	Challenge # survivors/total	LD ₅₀
—	wild type	—	0/10	—	<10
23	PM1B1	guaB	10/10, 10/10, 10/10	9/10, 9/10	4.3 x 106
11	PM1D1	dsbB	10/10, 5/10	10/10, 5/5	8.4 x 104
3	PM1BD7	atpG	5/5, 10/10	10/10	>3 x 105
74	PM1BE11	yhcJ (HI0145)	10/10	5/10	>2 x 105
70	PM1BF6	yabK (HI020)	3/5, 8/10	9/9	>2 x 105
19	PM2G8	fhaC	4/5, 9/10	9/9	>4 x 105
76	PM3C9	yiaO (HI0146)	3/5	—	>6 x 105
118	PM3G11	UnkO	4/5, 10/10	10/10	>3 x 105
31	PM7B4	iroA (UnkB)	0/5	—	—
17	PM4C6	fhaB (fhaB2)	2/5, 10/10, 9/10	10/10, 9/9	>3 x 106
9	PM4G10-T9	dnaA	4/5	—	>5 x 105
1	PM4D5-T5	atpB	5/5	—	>4 x 105
53	PM4D5-T1	UnkC2	5/5	—	>4 x 105
15	PM4F2	fhaB (fhaB1)	3/5, 6/10, 10/10	6/6, 10/10	>3 x 105
41	PM5F7	mreB	4/5	—	1 x 103
7	PM5E2	devB	0/5, 3/10	2/3	ND
68	PM6H5-T1	xylA	5/5	—	>3 x 105
78	PM6H8	yigF (HI0719)	5/5, 9/10	9/9	>3 x 105
108	PM7D12	pnp	5/5, 9/10	9/9	—
51	PM8C1R1-T2	UnkC1	5/5	—	~6 x 105

Nucleotide SEQ ID NO:	Representative Isolate	PossibleGene Function	Vaccination # survivors/total	Challenge # survivors/total	LD ₅₀
5	37 PM8C1-T3	mgIB	5/5		-6 x 105
	58 PM8C1R1-T6	UnkD1	5/5		-6 x 105
	45 PM10H7	purF (HI1207)	3/5, 8/10, 8/10	8/8, 8/8	>3 x 105
	25 PM10H10-T2	HI1501	5/5		>1 x 104
	72 PM11G8-T2	ygiK	5/5		>2.4 x 103
	21 PM11G8-T4	greA	5/5		>2.4 x 103
	84 PM12H6	yyam (HI0687)	3/5, 0/10		-2.2 x 103
	33 PM15G8-T2	kdtB	5/5		>1.2 x 105
10	116 PM15G8-T1	UnkK	5/5		>1.2 x 105
	104 PM16G11-T1	hmbR	3/5		>1.9 x 105
	29 PM16G11-T2	hxuC	3/5		>1.9 x 105
	35 PM16H8	lgtC	5/5, 10/10	10/10	>2.4 x 105
15	80 PM16H3	yleA (HI0019)	5/5, 10/10		> 2.0 x 105
	49 PM17H6-T1	sopE	4/5		-6 x 105
	120 PM17H6	UnkP	4/5		-6 x 105
	5 PM18F5-T8	capSE	5/5		>2.4 x 105
20	82 PM18F5-T10	yojB (HI0345)	5/5		>2.4 x 105
	13 PM19A1	exbB	5/5, 10/10	10/10	>1.2 x 105
	112 PM19D4	rci	5/5, 8/10	8/8	-1.6 x 105
	39 PM20A12	mioC (HI0669)	3/5, 8/10	8/8	-2 x 104
	60 PM20C2	UnkD2	5/5, 10/10	10/10	>8.2 x 106

Example 4
Cloning and Identification of Genes Required for *P. multocida* Virulence

25 Each transposon mutant which was verified to be attenuated was analyzed further to determine the identity of the disrupted open reading frame. DNA from each mutant was amplified, purified, and digested with restriction enzymes that were known not to cut within the transposon and generally produced 4-8 kb fragments that hybridized with the transposon. Using selection for kanamycin resistance
30 encoded by the transposon, at least one fragment for each transposon mutant was cloned.

35 Southern hybridization with multiple restriction enzymes was performed for each attenuated mutant using a labeled 1.8 kb *Mlu*I fragment from pLOF/Km as a probe to identify a suitably sized fragment for cloning. The mini-Tn10 element and flanking DNA from each mutant was cloned into pUC19 and the flanking sequence determined using internal primers TEF32 and TEF40, primer walking and in some cases universal pUC-19 primers.

TEF-32	GGCAGAGCATTACGCTGAC	SEQ ID NO: 95
TEF-40	GTACCGGCCAGGCAGCCACGCGTATT	SEQ ID NO:96

Sequencing reactions were performed using the BigDye™ Dye Terminator Chemistry
5 kit from PE Applied Biosystems (Foster City, CA) and run on an ABI Prism 377
DNA Sequencer. Double stranded sequence for putative interrupted open reading
frames was obtained for each clone. Sequencer 3.0 software (Genecodes, Corp., Ann
Arbor, MI) was used to assemble and analyze sequence data. GCG programs
[Devereux, *et al.*, 1997. Wisconsin Package Version 9.0, 9.0 ed. Genetics Computer
10 Group, Inc., Madison] were used to search for homologous sequences in currently
available databases.

In 37% of the clones that were identified as being attenuated, there
were multiple insertions of the mini-Tn10 transposable element. Each insertion
including its flanking sequence was cloned individually into pGP704 and mated into
15 the wild-type strain to produce new mutants of *P. multocida*, each carrying only one
of the multiple original insertions. Individual mutants were retested individually to
determine the insertion responsible for the attenuated phenotype. The nucleotide
sequence of the disrupted, predicted open reading frame was determined by
sequencing both strands, and the predicted amino acid sequence was used to search
20 currently available databases for similar sequences. Sequences either matched known
genes, unknown genes, and hypothetical open reading frames previously sequenced or
did not match any previously identified sequence. For those genes having homology
to previously identified sequences, potential functions were assigned as set out in
Table 1.

25

Example 5
Identification of Related Genes in Other Species

In separate experiments, STM was also performed using *Actinobacillus pleuropneumoniae* (App). One of the App strains contained an insertion in a gene that
30 was sequenced (SEQ ID NO: 97) and identified as a species homolog of the *P. multocida* *atpG* gene. This result suggested the presence in other bacterial species of

homologs to previously unknown *P. multocida* genes that can also be mutated to produce attenuated strains of the other bacterial species for use in vaccine compositions. In order to determine if homologs of other *P. multocida* genes exists in other bacterial species, Southern hybridization was performed on genomic DNA from other species using the *A. pleuropneumoniae* *atgG* gene as a probe.

5 *Actinobacillus pleuropneumoniae*, *Pasteurella haemolytica* (Ph), *P. multocida*, and *Haemophilus somnis* (Hs) genomic DNA was isolated using the CTAB method and digested with *Eco*RI and *Hind*III for two hours at 37°C. Digested DNA was separated on a 0.7% agarose gel at 40V in TAE buffer overnight. The gel
10 was immersed sequentially in 0.1 M HCl for 30 minutes, twice in 0.5 M NaOH/1.5 M NaCl for 15 minutes each, and twice in 2.5 M NaCl/1 M Tris, pH 7.5. The DNA was transferred to nitrocellulose membranes (Amersham Hybond N⁺) overnight using 20X SSC buffer (3 M NaCl/0.3 M sodium citrate). The DNA was crosslinked to the membrane using a UV Stratalinker on autocrosslink setting (120 millijoules). The
15 membrane was prehybridized in 5X SSC/ 1% blocking solution/0.1% sodium lauroyl sarcosine/0.02% SDS at 50°C for approximately seven hours and hybridized overnight at 50°C in the same solution containing a PCR generated *atgG* probe.

15 The probe was prepared using primers DEL-1389 (SEQ ID NO: 98) and TEF-46 (SEQ ID NO: 99) in a with a GeneAmp XL PCR kit in a GeneAmp PCR System 2400. Template was genomic *A. pleuropneumoniae* DNA.

DEL-1389	TCTCCATTCCCTTGCTGCGGCAGGG	SEQ ID NO: 98
TEF-46	GGAATTACAGCCGGATCCGGG	SEQ ID NO: 99

25 The PCR was performed with an initial heating step at 94°C for five minutes, 30 cycles of denaturation t 94°C for 30 sec, annealing at 50°C for 30 sec, and elongation at 72°C for three minutes, and a final extension step at 72°C for five minutes. The amplification products were separated on an agarose gel, purified using a QIAquick gel purification kit (QIAGEN), and labeled using a DIG-High Primer kit (Boehringer
30 Mannheim). The blot was removed from the hybridization solution and rinsed in 2X

SSC and washed two times for five minutes each wash in the same buffer. The blot was then washed two times for 15 minutes each in 0.5X SSC at 60°C. Homologous bands were visualized using a DIG Nucleic Acid Detection Kit (Boehringer Mannheim).

5 Single bands were detected in *Pasteurella haemolytica*, *Haemophilus somnus* and *A. pleuropneumoniae* using EcoRI digested DNA. Two bands were detected using EcoRI digested DNA from *Pasteurella multocida*.

10 **Example 6**
Construction of a Library of Tagged-Transposon *P. multocida* Mutants

Transposon mutagenesis using pLOF/Km has previously been reported to be functional and random in *A. pleuropneumoniae* [Tascon, et al., *J Bacteriol.* 175:5717-22 (1993)]. To construct tagged transposon mutants of *A. pleuropneumoniae*, each of 96 *E. coli* S17-1:λpir transformants containing pre-selected tagged plasmids (pTEF-1:[NK]₃₅) was used in conjugative matings to generate transposon mutants of *A. pleuropneumoniae* strain AP225, a serotype 1 spontaneous nalidixic acid resistant mutant derived from an in vivo passaged ATCC 27088 strain. *A. pleuropneumoniae* strains were grown on Brain Heart Infusion (BHI) (Difco Laboratories, Detroit, MI) media with 10 µg/ml B-nicotinamide adenine dinucleotide (V¹⁰), (Sigma, St. Louis, Missouri) at 37°C and in 5% CO₂ when grown on plates. *E. coli* S17-1:λpir (λpir, *recA*, *thi*, *pro*, *hsdR(r_k-,m_k+)*, RP4-2, (Tc^R::Mu), (Km^R::Tn7), [Tmp^R], [Sm^R]) was propagated at 37°C in Luria-Bertani (LB) medium. Antibiotics when necessary were used at 100 µg/ml ampicillin (Sigma), 50 µg/ml nalidixic acid (N⁵⁰)(Sigma), and 50 (K⁵⁰) or 100 (K¹⁰⁰) µg/ml of kanamycin (Sigma).
20
25 Matings were set up by growing each *E. coli* S17-1:λpir/pTEF1:[NK]₃₅ clone and the AP225 strain to late log phase. A 50 µl aliquot of culture for each tagged-pTEF-1 clone was mixed with 150 µl of the APP225 culture, and then 50 µl of each mating mixture was spotted onto 0.22 µM filters previously placed onto BHIV¹⁰ plates containing 100 µM IPTG and 10 mM MgSO₄. Following overnight incubation at 37°C with 5% CO₂, mating mixtures were washed off of each filter into 2 ml of PBS and 200 µl of each was plated onto BHIV¹⁰N⁵⁰K¹⁰⁰ plates. After selective
30

overnight growth, colonies were assembled into microtiter plates by toothpick transfer into 200 μ l BHIV¹⁰N⁵⁰K⁵⁰ making sure that each well in a microtiter plate always contained a transposon mutant with the same sequence tag. Following overnight growth, 50 μ l of 75% glycerol was added to each well and plates were stored frozen at 5 -80°C.

APP does not appear to have as much bias towards multiple insertions of the mini-Tn10 element as did *P. multocida*. Only approximately 3% of the mutants were determined to contain multiple insertions, which is in agreement with the 4% previously reported [Tascon, *et al.*, *J Bacteriol.* 175:5717-22 (1993)]. A problem in 10 APP consisted of identifying numerous mutants (discussed below) containing insertions into 23S RNA regions: 28 total mutants with insertions into 13 unique sites. This may indicate that 23S RNA contains preferential insertion sites and that the growth of APP is affected by these insertions enough to result in differential survival within the host. Southern blot analysis using an APP 23S RNA probe suggests that 15 APP may contain only three ribosomal operons as compared to five in *H. influenzae* [Fleischmann, *et al.*, *Science* 269:496-512 (1995)] and seven complete operons in *E. coli* [Blattner, *et al.*, *Science* 277:1453-1474 (1997)]. This site preference and its effect on growth rate may be a significant barrier to "saturation mutagenesis" since a significant number of clones will contain insertions into these rRNAs and large 20 volume screening will be necessary to obtain additional unique attenuating mutations.

Example 7 Porcine Screening for Attenuated *A. pleuropneumoniae* Mutants

Twenty pools of *A. pleuropneumoniae* transposon mutants, containing 25 a total of approximately 800 mutants, were screened using a porcine intratracheal infection model. Each pool was screened in two separate animals.

Frozen plates of pooled *A. pleuropneumoniae* transposon mutants were removed from -80°C storage and subcultured by transferring 20 μ l from each well to a new 96 well round bottom plate (Corning Costar, Cambridge, MA, USA) containing 30 180 μ l of BHIV¹⁰N⁵⁰K⁵⁰. Plates were incubated without shaking overnight at 37°C in

5% CO₂. Overnight plates were then subcultured by transferring 10 µl from each well to a new flat bottomed 96 well plate (Corning Costar) containing 100 µl of BHIV¹⁰ per well and incubating at 37°C with shaking at 150 rpm. The OD₅₆₂ was monitored using a microtiter plate reader. At an OD₅₆₂ of approximately 0.2 to 0.25, each plate
5 was pooled to form the "input pool" by combining 100 µl from each of the wells of the microtiter plate. The culture was diluted appropriately in BHI to approximately 2 X 10⁶ CFU/ml. For each diluted pool, 4.0 ml was used to infect 10-20 kg SPF pigs (Whiteshire-Hamroc, Albion, IN) by intratracheal administration using a tracheal tube. At approximately 20 hours post-infection, all surviving animals were euthanized and
10 the lungs removed. Lavage was performed to recover surviving bacteria by infusing 150 mls of sterile PBS into the lungs, which were then massaged to distribute the fluid. The lavage fluid was recovered, and the process was repeated a second time. The lavage fluid was centrifuged at 450 x g for 10 minutes to separate out large debris. Supernatants were then centrifuged at 2,800 x g to pellet the bacteria. Pellets
15 were resuspended in 5 mls BHI and plated in dilutions ranging from 10² to 10⁻⁵ onto BHIV¹⁰N⁵⁰K⁵⁰ plates. Following overnight growth, at least 100,000 colonies were pooled in 10 mls BHI broth to form the "recovered pools". A 0.7 ml portion of each recovered pool was used to prepare genomic DNA by the CTAB method [Wilson, *In*
Ausubel, *et al.*, (eds.), Current Protocols in Molecular Biology, vol. 1. John Wiley and Sons, New York, p. 2.4.1-2.4.5 (1997)].
20

Recovery from the animals routinely was in the 10⁸ CFU range from lung lavage.

Dot blots were performed and evaluated both by visual inspection and by semi-quantitative analysis as described previously. All hybridizations and
25 detections were performed as described. Briefly, probes were prepared by a primary PCR amplification, followed by agarose gel purification of the desired product and secondary PCR amplification incorporating dig-dUTP. Oligonucleotides including TEF5, TEF6, TEF24, TEF25, TEF48 and TEF62, were synthesized by Genosys Biotechnologies (The Woodlands, TX). Primers TEF69, TEF65, and TEF66 were also
30 used for inverse PCR reactions and sequencing.

TEF69	GACGTTCCCGTTGAATATGGCTC	SEQ ID NO: 166
TEF65	GCCGGATCCGGGATCATATGACAAGA	SEQ ID NO: 167
TEF66	GACAAGATGTGTATCCACCTAAC	SEQ ID NO: 168

5

The labeled PCR product was then digested with *Hind*III to separate the constant primer arms from the unique tag region. The region containing the labeled variable tag was excised and the entire gel slice was then dissolved and denatured in DIG EasyHyb. Dot blots were prepared and detected using the standard 10 CSPD detection protocol. Film exposures were made for visual evaluation, and luminescent counts per second (LCPS) were determined for each dot blot sample. The LCPS_{input} / LCPS_{recovered} ratio for each mutant was used to determine mutants likely to be attenuated.

Clones selected as being present in the input pool but highly reduced in 15 the recovered pool were selected for further study. Additional clones with questionable input/recovered ratios were also selected after visually evaluating films made from the dot blots. A total of 110 clones were selected.

20

Example 8 Identification of *A. pleuropneumoniae* Virulence Genes

A partial flanking sequence was determined for each of the 110 25 mutants by inverse PCR and direct product sequencing. Inverse PCR was used to generate flanking DNA products for direct sequencing as described above. Sequencing reactions were performed using the BigDye™ Dye Terminator Chemistry kit from PE Applied Biosystems (Foster City, CA) and run on an ABI Prism 377 30 DNA Sequencer. Sequencher 3.0 software (Genecodes, Corp., Ann Arbor, MI) was used to assemble and analyze sequence data. GCG programs [Devereux and Haeberli, Wisconsin Package Version 9.0, 9.0 ed. Genetics Computer Group, Inc., Madison (1997)] were used to search for homologous sequences in currently available databases.

Table 2 shows the *A. pleuropneumoniae* genes identified and extent to which open reading frames were determinable. Sequence identification numbers are provided for nucleotide sequences as well as deduced amino acid sequences where located.

5

Table 2
***A. pleuropneumoniae* Open Reading Frames**

<u>Complete Open Reading Frame</u>		<u>NO Start Codon - Stop Codon</u>	
10	atpH	SEQ ID NO: 134	dksA
	aptG	SEQ ID NO: 132	dnaK
	exbB	SEQ ID NO: 140	HI0379
	OmpP5	SEQ ID NO: 152	
15	OmpP5-2	SEQ ID NO: 150	<u>NO Start Codon - NO Stop Codon</u>
	tig	SEQ ID NO: 160	pnp
	fkpA	SEQ ID NO: 142	apvA-or 1
	hupA	SEQ ID NO: 146	apvA-or 2
	rpmF	SEQ ID NO: 158	apvB apvD
<u>Start Codon - NO Stop Codon</u>		<u>RNA or Noncoding Sequences</u>	
20	lpdA	SEQ ID NO: 148	tRNA-leu
	potD	SEQ ID NO: 156	SEQ ID NO: 162
	yaeE	SEQ ID NO: 164	tRNA-glu
	apvC	SEQ ID NO: 128	SEQ ID NO: 163

25

The putative identities listed in Table 3 (below, Example 9) were assigned by comparison with bacterial databases. The 110 mutants represented 35 groups of unique transposon insertions. The number of different mutations per loci varied, with some clones always containing an insertion at a single site within an ORF to clones containing insertions within different sites of the same ORF. Three multiple insertions were detected in the 110 mutants screened as determined by production of multiple PCR bands and generation of multiple sequence electropherograms.

30

Example 9
Competition Challenge of *A. pleuropneumoniae*
Mutants with Wild Type APP225

A representative clone from each of the unique attenuated mutant

5 groups identified above that was absent or highly reduced in the recovered population
was isolated from the original pool plate and used in a competition challenge
experiment with the wild type strain (AP225) to verify the relative attenuation caused
by the transposon mutation. Mutant and wild type strains were grown in BHIV¹⁰ to an
OD₅₉₀ of 0.6 – 0.9. Approximately 5.0 x 10⁶ CFU each of the wild type and mutant
10 strains were added to 4 mls BHI. The total 4 ml dose was used infect a 10-20 kg SPF
pig by intratracheal administration with a tracheal tube. At approximately 20 hours
post-infection, all surviving animals were euthanized and the lungs removed. Lung
lavages were performed as described above. Plate counts were carried out on
BHIV¹⁰N⁵⁰ and BHIV¹⁰N⁵⁰K¹⁰⁰ to determine the relative numbers of wild type to
15 mutant in both the input cultures and in the lung lavage samples. A Competitive
Index (CI) was calculated as the [mutant CFU / wild type CFU]_{input} / [mutant CFU /
wild type CFU]_{recovered}.

20 Of the 35 potential transposon mutants, 22 were significantly
attenuated, having a competitive index (CI) of less than 0.2. A transposon mutant that
did not seem to be attenuated based on the STM screening results was chosen from
one of the pools as a positive control. This mutant had a CI in vivo of approximately
0.6. An in vitro competition was also done for this mutant resulting in a CI of 0.8.
The mutant was subsequently determined to contain an insertion between 2
phenylalanine tRNA's.

25 Competitive indices for unique attenuated single-insertion mutants are
listed in Table 3. Competitive indices for *atpG*, *pnp*, and *exbB* App mutants indicated
that the mutants were unable to compete effectively with the wild type strains and
were therefore attenuated.

Table 3
Virulence and Proposed Function of *A. pleuropneumoniae* Mutants

	Mutant	Similarity	Putative or Known Functions	C.I.
5	AP20A6	<i>atpH</i>	ATP synthase	.009
	AP7F10	<i>atpG</i>	ATP synthase	.013
	AP17C6	<i>lpdA</i>	dihydrolipoamide dehydrogenase	.039
10	AP11E7	<i>exbB</i>	transport of iron compounds	.003,.003,.006
	AP3H7	<i>potD</i>	Spermidine/putrescine transport	.308
	AP8H6	<i>OmpP5</i>	Adhesin / OmpA homolog	.184
	AP18H8	<i>OmpP5-2</i>	Adhesin / OmpA homolog	.552
	AP13E9	<i>tig</i>	Peptidyl-prolyl isomerase	.050
	AP13C2	<i>fkpA</i>	Peptidyl-prolyl isomerase	<.001
15	AP15C11	<i>pnp</i>	Polynucleotide phosphorylase	.032
	AP18F12	<i>hupA</i>	Histone – like protein	.001
	AP20F8	<i>dksA</i>	Dosage dependent suppressor of dnaK mutations	.075
	AP5G4	<i>dnaK</i>	Heat shock protein – molecular chaperone	.376
20	AP17C9	<i>tRNA-leu</i>	Protein Synthesis	.059
	AP5D6	<i>tRNA-glu</i>	Protein Synthesis	.055
	AP18B2	<i>rpmF</i>	Protein Synthesis	.112
25	AP10E7	<i>yaeA</i>	Unknown	.001
	AP19A5	HI0379	Unknown	.061
	AP10C10	<i>apvA</i>	Unknown	.157
	AP18F5	<i>apvB</i>	Unknown	.103
	AP2A6	<i>apvC</i>	Unknown	.091
30	AP2C11	<i>apvD</i>	Unknown	.014

Accuracy of the CI appeared to be very good as the *exbB* mutant was competed within three different animals yielding CI's of 0.003, 0.003 and 0.006. The use of a Competitive Index number to assign attenuation based upon one competition in a large animal study was further confirmed based on preliminary vaccination results in pigs with 7 mutants (n=8) described below in Example 11.

Example 10
Characterization of Attenuated *A. pleuropneumoniae* Virulence Genes

The *A. pleuropneumoniae* genes identified represent four broad functional classes: biosynthetic enzymes, cellular transport components, cellular regulation components and unknowns.

The *atpG* gene, encoding the F₁-γ subunit of the F₀F₁ H⁺-ATPase complex, can function in production of ATP or in the transport of protons by hydrolyzing ATP. A related *atpG* attenuated mutant was also identified in *P. multocida*. Another *atp* gene, *atpH*, that encodes the F₁ δ subunit was also identified. Phenotypes of *atp* mutants include non-adaptable acid-sensitivity phenotype [Foster, *J Bacteriol.* 173:6896-6902 (1991)], loss of virulence in *Salmonella typhimurium* [Garcia del Portillo, *et al.*, *Infect Immun.* 61:4489-4492 (1993)] and *P. multocida* (above) and a reduction in both transformation frequencies and induction of competence regulatory genes in *Haemophilus influenzae* Rd [Gwinn, *et al.*, *J Bacteriol.* 179:7315-20 (1997)].

LpdA is a dihydrolipoamide dehydrogenase that is a component of two enzymatic complexes: pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase. While the relationship to virulence is unknown, production of LpdA is induced in *Salmonella typhimurium* when exposed to a bactericidal protein from human which may suggest that this induction may be involved in attempts to repair the outer membrane [Qi, *et al.*, *Mol Microbiol.* 17:523-31 (1995)].

Transport of scarce compounds necessary for growth and survival are critical in vivo. ExbB is a part of the TonB transport complex [Hantke, and Zimmerman, *Microbiology Letters.* 49:31-35 (1981)], interacting with TonB in at least two distinct ways [Karlsson, *et al.*, *Mol Microbiol.* 8:389-96 (1993), Karlsson, *et al.*, *Mol Microbiol.* 8:379-88 (1993)]. Iron acquisition is essential for pathogens. In this work, attenuated *exbB* mutants in both APP and *P. multocida* have been identified. Several TonB-dependent iron receptors have been identified in other bacteria [Biswas, *et al.*, *Mol. Microbiol.* 24:169-179 (1997), Braun, *FEMS Microbiol Rev.* 16:295-307 (1995), Elkins, *et al.*, *Infect Immun.* 66:151-160 (1998), Occhino, *et*

al., Mol Microbiol. 29:1493-507 (1998), Stojilkovic and Srinivasan, *J Bacteriol.* 179:805-12 (1997)]. *A. pleuropneumoniae* produces 2 transferrin-binding proteins, which likely depend on the ExbB/ExbD/TonB system, for acquisition of iron. PotD is a periplasmic binding protein that is required for spermidine (a polyamine) transport [Kashiwagi, *et al.*, *J Biol Chem.* 268:19358-63 (1993)]. Another member of the *Pasteurellaceae* family, *Pasteurella haemolytica*, contains a homologue of *potD* (Lpp38) that is a major immunogen in convalescent or outer membrane protein vaccinated calves [Pandher and Murphy, *Vet Microbiol.* 51:331-41 (1996)]. In *P. haemolytica*, PotD appeared to be associated with both the inner and outer membranes. The role of PotD in virulence or in relationship to protective antibodies is unknown although previous work has shown *potD* mutants of *Streptococcus pneumoniae* to be attenuated [Polissi, *et al.*, *Infect. Immun.* 66:5620-9 (1998)].

Relatively few "classical virulence factors," such as adhesins or toxins with the exception of homologues to OMP P5 of *Haemophilus influenzae*, were identified. *H. influenzae* OMP P5 is a major outer membrane protein that is related to the OmpA porin family of proteins [Munson, *et al.*, *M Infect Immun.* 61:4017-20 (1993)]. OMP P5 in nontypeable *Haemophilus influenzae* has been shown to encode a fimbrial subunit protein expressed as a filamentous structure [Sirakova, *et al.*, *Infect Immun.* 62:2002-20 (1994)] that contributes to virulence and binding of both mucin and epithelial cells [Miyamoto and Bakaletz, *Microb Pathog.* 21:343-56 (1996), Reddy, *et al.*, *Infect Immun.* 64:1477-9 (1996), Sirakova, *et al.*, *Infect Immun.* 62:2002-20 (1994)]. A significant finding was identification of two distinct ORF's that appear to encode OMP P5 homologues. This is also the case with two very similar proteins, MOMP and OmpA2 from *Haemophilus ducreyi*. It remains to be determined whether both are functionally involved in the production of fimbriae and whether the presence of two such ORFs represents a divergent duplication with redundant or complementing functions. Interestingly, the two OMP P5 mutants seem to have disparate CI values, suggesting a difference in essentiality or functionality for only one copy. OMP P5 has been shown to undergo molecular variation during chronic infections [Duim, *et al.*, *Infect Immun.* 65:1351-1356 (1997)], however, this

appears to be restricted to a single gene undergoing point mutations resulting in amino acid changes rather than "type switching" due to differential expression of multiple genes.

Protein folding enzymes are important accessories for the efficient folding of periplasmic and extracellular proteins, and two genes were identified whose products have peptidyl-prolyl isomerase activity: *fkpA* and *tig* (trigger factor). FkpA is a periplasmic protein that is a member of the FK506-binding protein family [Horne and Young, *Arch Microbiol.* 163:357-65 (1995); Missiakas, *et al.*, *Mol Microbiol.* 21:871-84 (1996)]. FkpA has been shown to contribute to intracellular survival of *Salmonella typhimurium* [Horne, *et al.*, *Infect Immun.* 65:806-10 (1997)] and a *Legionella pneumophila* homolog, *mip* [Engleberg, *et al.*; *Infect Immun.* 57:1263-1270 (1989)], is responsible for virulence and infection of macrophages [Cianciotto, *et al.*, *J. Infect. Dis.* 162:121-6 (1990); Cianciotto, *et al.*, *Infect. Immun.* 57:1255-1262 (1989)]. Tig, or trigger factor [Crooke and Wickner, *Proc. Natl. Acad. Sci. USA.* 84:5216-20 (1987), Guthrie, and Wickner, *J Bacteriol.* 172:5555-62 (1990), reviewed in Hesterkamp, and Bukau., *FEBS Lett.* 389:32-4 (1996)], is a peptidyl prolyl isomerase containing a typical FKBP region [Callebaut and Mornon, *FEBS Lett.* 374:211-215 (1995)], but is unaffected by FK506 [Stoller, *et al.*, *EMBO J.* 14:4939-48 (1995)]. Tig has been shown to associate with the ribosomes and nascent polypeptide chains [Hesterkamp, *et al.*, *Proc Natl Acad Sci USA* 93:4437-41 (1996), Stoller, *et al.*, *EMBO J.* 14:4939-48 (1995)]. Possible roles include an unknown influence on cell division [Guthrie, and Wickner, *J Bacteriol.* 172:5555-62 (1990)] in *E. coli*, a role in the secretion and activation of the *Streptococcus pyogenes* cysteine proteinase [Lyon, *et al.*, *EMBO J.* 17:6263-75 (1998)] and survival under starvation conditions in *Bacillus subtilis* [Gothel, *et al.*, *Biochemistry* 37:13392-9 (1998)].

Bacterial pathogens employ many mechanisms to coordinately regulate gene expression in order to survive a wide variety of environmental conditions within the host. Differences in mRNA stability can modulate gene expression in prokaryotes [Belasco and Higgins, *Gene* 72:15-23 (1988)]. For example, *rnr* (*vacB*) is required for expression of plasmid borne virulence genes in *Shigella flexneri* [Tobe, *et al.*, *J*

Bacteriol. 174:6359-67 (1992)] and encodes the RnaseR ribonuclease [Cheng, *et al.*, *J. Biol. Chem.* 273:14077-14080 (1998)]. PNP is a polynucleotide phosphorylase that is involved in the degradation of mRNA. Null *pnp / rnr* mutants are lethal, suggesting a probable overlap of function. It therefore is possible that both *rnr* and *pnp* are involved in the regulation of virulence gene expression. A *pnp* mutant of *P. multocida* is avirulent in a mouse septicemic model (Example 2)]. Other *pnp*-associated phenotypes include competence deficiency and cold sensitivity in *Bacillus subtilis* [Wang and Bechhofer, *J Bacteriol.* 178:2375-82 (1996)].

HupA is a bacterial histone-like protein, which in combination with HupB constitute the HU protein in *E. coli*. Reports have suggested that *hupA* and *hupB* single mutants do not demonstrate any observable phenotype [Huisman, *et al.*, *J Bacteriol.* 171:3704-12 (1989), Wada, *et al.*, *J Mol Biol.* 204:581-91 (1988)], however, *hupA-hupB* double mutants have been shown to be cold sensitive, sensitive to heat shock and blocked in many forms of site-specific DNA recombination [Wada, *et al.*, *J Mol Biol.* 204:581-91 (1988), Wada, *et al.*, *Gene.* 76:345-52 (1989)]. One limited data previously indicated that *hupA* is directly involved in virulence [Turner, *et al.*, *Infect Immun.* 66:2099-106 (1998)]. The mechanism of *hupA* attenuation remains unknown.

DnaK is a well known and highly conserved heat shock protein involved in regulatory responses to various stressful environmental changes [reviewed in Lindquist and Craig, *Annu Rev Genet.* 22:631-77 (1988)]. DnaK is also one of the most significantly induced stress proteins in *Yersinia enterocolitica* after being phagocytosed by macrophages [Yamamoto, *et al.*, *Microbiol Immunol.* 38:295-300 (1994)] and a *Brucella suis dnaK* mutant failed to multiply within human macrophage-like cells [Kohler, *et al.*, *Mol Microbiol.* 20:701-12 (1996)]. In contrast, another intracellular pathogen, *Listeria monocytogenes*, did not show induction of *dnaK* after phagocytosis [Hanawa, *et al.*, *Infect Immun.* 63:4595-9 (1995)]. A *dnaK* mutant of *Vibrio cholera* affected the production of ToxR and its regulated virulence factors in vitro but similar results were not obtained from in vivo grown cells [Chakrabarti, *et al.*, *Infect Immun.* 67:1025-1033 (1999)]. The CI of *A.*

pleuropneumonia dnaK mutant was higher than most of the attenuated mutants although still approximately half of the positive control strain.

DksA is a dosage dependent suppressor of filamentous and temperature-sensitive growth in a *dnaK* mutant of *E. coli* [Kang and Craig, *J Bacteriol.* 172:2055-64 (1990)]. There is currently no defined molecular function for DksA, but the gene has been identified as being critical for the virulence of *Salmonella typhimurium* in chickens and newly hatched chicks [Turner, *et al.*, *Infect Immun.* 66:2099-106 (1998)]. In that work, it was noted that the *dksA* mutant did not grow well with glucose or histidine but did grow well with glutamine or glutamate as the sole carbon source. This observation may indicate that the *dksA* mutant is somehow impaired in the biosynthesis of glutamate [Turner, *et al.*, *Infect Immun.* 66:2099-106 (1998)].

Three genes were identified that have roles in protein synthesis: tRNA-leu, tRNA-glu and *rpmF*. Excluding protein synthesis, tRNA's also have a wide variety of functional roles in peptidoglycan synthesis [Stewart, *et al.*, *Nature* 230:36-38 (1971)], porphyrin ring synthesis [Jahn, *et al.*, *Trends Biochem Sci.* 17:215-8 (1992)], targeting of proteins for degradation [Tobias, *et al.*, *Science* 254:1374-7 (1991)], post-translational addition of amino acids to proteins [Leibowitz and Soffer, *B.B.R.C.* 36:47-53 (1969)] and mediation of bacterial-eukaryotic interactions [Gray, *et al.*, *J Bacteriol.* 174:1086-98 (1992), Hromockyj, *et al.*, *Mol Microbiol.* 6:2113-24 (1992)]. More specifically, tRNA-leu is implicated in transcription attenuation [Carter, *et al.*, *Proc. Natl. Acad. Sci. USA* 83:8127-8131 (1986)], lesion formation by *Pseudomonas syringae* [Rich and Willis, *J Bacteriol.* 179:2247-58 (1997)] and virulence of uropathogenic *E. coli* [Dobrindt, *et al.*, *FEMS Microbiol Lett.* 162:135-141 (1998), Ritter, *et al.*, *Mol Microbiol.* 17:109-21 (1995)]. It is unknown whether the tRNA that we have identified represents a minor species of tRNA-leu in *A. pleuropneumoniae*. Regardless, it is possible that tRNA-leu may have any one of a wide range of functions. RpmF is a ribosomal protein whose gene is also part of an operon containing fatty acid biosynthesis enzymes in *E. coli*. Further work will be required to indicate if this is the case in *A. pleuropneumoniae*, although the same

clustering of *fab* genes and *rpmF* occurs in *Haemophilus influenzae* [Fleischmann, *et al.*, *Science* 269:496-512 (1995)]. The expression of the *fab* genes is not necessarily dependent on transcripts originating upstream of *rpmF* as there has been a secondary promoter identified within *rpinF* [Zhang and Cronan, Jr., *J Bacteriol.* 180:3295-303 (1998)].

The final class of attenuated mutants includes mutations within genes of unknown function or genes that have not been previously identified. Homologs of *yaeA* and HI0379 have previously been identified in *Escherichia coli* [Blattner, *et al.*, *Science* 277:1453-1474 (1997)] and *Haemophilus influenzae* [Fleischmann, *et al.*, *Science* 269:496-512 (1995)], respectively. The remaining unknowns have been designated *Actinobacillus pleuropneumoniae* virulence genes (*apv*). The *apvC* gene shows significant similarity to HI0893, however, the proposed similarity of HI0893 as a transcriptional repressor similar to the fatty acid response regulator Bm3R1 [Palmer, *J Biol Chem.* 273:18109-16 (1998)] is doubtful. The *apvD* gene is also most similar to a putative membrane protein (b0878) with unknown function from *E. coli* [Blattner, *et al.*, *Science* 277:1453-1474 (1997)]. Two other unknowns, *apvA* and *apvB* had no significant matches in the public databases.

Example 11
Safety and Efficacy of *A. pleuropneumoniae* Mutants

Nine groups (n=8) of SPF pigs (4-5 weeks old, 3-10 kg) were used to determine the safety and efficacy of seven *A. pleuropneumoniae* mutants as live attenuated vaccine strains. Seven groups were infected intranasally with 10^{10} CFU of each mutant on day 1. One group was vaccinated on days 1 and 15 with the commercially available vaccine Pleuromune (Bayer), and one naive group was not vaccinated. On day 29, all groups were challenged intranasally with $1-5 \times 10^5$ CFU per pig of wild type APP225. All surviving animals were euthanized and necropsied on day 42 of the study. Results are shown in Table 4.

Table 4
Efficacy of *A. pleuropneumoniae* Mutants

	<u>Vaccine</u>	% Mortality following intranasal challenge	
		<u>Vaccination</u>	<u>Challenge</u>
5	Pleuromune	0	37.5
	exbB	0	0
	tig	12.5	0
	fkpA	12.5	0
	HI0385	50.0	0
10	pnp	0	0
	yaeE	0	0
	atpG	0	0
	None	N/A	50.0

15 The *exbB*, *atpG*, *pnp*, and *yaeA* mutants caused no mortality when administered at a dosage of 10^{10} CFU intranasally. The *fkpA* and *tig* mutant groups had one death each and the HI0379 group (highest CI of the 7 mutants tested shown in Example 9) had four deaths. Wildtype LD₅₀ using this model was generally 1×10^7 CFU, indicating that each of these mutants is at least 100 fold attenuated and that there is a reasonable correlation between CI and attenuation.

20

Example 12
Identification of *P.(Mannheimia) haemolytica* Species Homologs

25 Based on the sequences of virulence genes identified in *P. multocida* and *A. pleuropneumoniae*, attempt were made to identify related genes, i.e., species homologs, in *P. (Mannheimia) haemolytica*. PCR was utilized with the degenerate primers shown below to attempt amplification of the *P. (Mannheimia) haemolytica* genes as indicated. Primer sequences, synthesized by Sigma-Genosys (The Woodlands, TX), include standard single letter designations, wherein B indicates

either (C,G or T), D indicates either (G,A or T), H indicates either (A,C or T), K indicates either (G or T), M indicates either (A or C), N indicates either (A,G,C or T), R indicates either (A or G), S indicates either (G or C), V indicates either (G, A, or C), W indicates either (A or T), and Y indicates either (C or T).

5

	atpG	TEF146	ATG GCN GGN GCN AAR GAR AT	SEQ ID NO: 176
		TEF148	GCN GCY TTC ATN GCN ACC AT	SEQ ID NO: 177
10	guaB	TEF240	GGN TTG ATY CAY AAA AAY ATG	SEQ ID NO: 178
		TEF243	TCT TTN GTR ATN GTN ACA TCR TG	SEQ ID NO: 179
	pnp	TEF141	GCS GGY AAA CCR CGT TGG GAT TGG	SEQ ID NO: 180
		TEF142	CRC CTA ARA TRT CTG AAA GCA CCA C	SEQ ID NO: 181
15	purF	TEF244	ATG TGY GGN ATY GTN GGN AT	SEQ ID NO: 182
		TEF247	CAT ATC AAT ACC ATA CAC ATT	SEQ ID NO: 183
20	yjgF	TEF162	GGN CCN TAY GTN CAR G	SEQ ID NO: 184
		TEF163	NGC NAC YTC NAC RCA	SEQ ID NO: 185

For amplification of initial degenerate PCR products, a 50 µl reaction was set up using 3.3X XL buffer II (PE Applied Biosystems), 200 µM dNTPs, 25 pmol each of the appropriate primers, 0.8 mM MgCl₂, 0.5 U rTth DNA polymerase, XL (PE Applied Biosystems) and approximately 1 µg of TF1 DNA.

25

Cycle conditions were 94°C for 1.5 min; followed by 35 cycles of 94°C for 15 s, 40-60°C for 60 s, 72°C for 1.5 min; and a final hold at 72°C for 5 min. Each PCR product was band purified from an agarose gel using the QIAGEN Gel Extraction Kit (QIAGEN, Valencia CA).

30

Sequencing reactions were performed using the BigDye™ Dye Terminator Chemistry kit from PE Applied Biosystems (Foster City, CA) and run on an ABI Prism 377 DNA Sequencer. Double stranded sequence for the open reading frame (ORF) for each clone was obtained. Sequencher 3.0 software (Genecodes, Corp., Ann Arbor, MI) was used to assemble and analyze sequence data. GCG programs were used to confirm the identity of the ORF by searching for homologous sequences in currently available databases.

35

The Vectorette Kit (Genosys Biotechnologies, The Woodlands, TX) was used to obtain additional flanking sequence for each of the genes. Vectorette libraries were prepared according to the manufacturer's suggested protocol. Perkin Elmer Applied Biosystems GeneAmp XL PCR Kit components were used to create the Vectorette PCR products with the following reaction conditions. A 50 µl reaction was set up using 3.3X XL buffer II (PE Applied Biosystems), 200 µM dNTPs, 25 pmol each of the appropriate primers(shown below), 0.8 mM MgCl₂, 0.5 U rTth DNA polymerase, XL (PE Applied Biosystems) and 1 µl of the appropriate vectorette library. Cycle conditions were 94°C for 1.5 min; followed by 35 cycles of 94°C for 20 s, 60°C for 45s, 72°C for 4 min; and a final hold of 72°C for 7 min. The second primer for each library was the manufacturer's vectorette primer.

Table 5

Gene	Vectorette library	Primer(s)
atpG	BglII, HindIII	TEF217 GAAGCCGCCATACGCTCTGGG SEQ ID NO: 186
	ClaI	TEF218 GTTGCTTCCTTGCCTGCACTGG SEQ ID NO: 187
5 guAB	EcoRI	TEF265 GGCTCAGAAACAATACCACTTCA SEQ ID NO: 188
	HindIII, TaqI	TEF268 GCACCAAAGCAGAATTGTCC SEQ ID NO: 189
10 pnp	ClaI, HincII	TEF219 GGTGATGATGTCGATGATAGTCCC SEQ ID NO: 190
	TaqI,	TEF220 GGC GTATTAGCCGTGATGCCAAC SEQ ID NO: 191
	BamHI	TEF286 GACCACTAGGCGATATGGACTT SEQ ID NO: 192
15 purF	TaqI	TEF271 ACCATCATAAATCGCCTGATT SEQ ID NO: 193 TEF292 ACCTGCGGCATCTTGTCC SEQ ID NO: 194
	HincII	TEF274 ACGGGTTTATTTCGCCTCTG SEQ ID NO: 195
	ClaI	TEF221 CGCCGGTTTCAGGATTACGGG SEQ ID NO: 196
yjgF	EcorV	TEF281 CTGAACAAACGTGAAAGCCAT SEQ ID NO: 197

Vectorette PCR products were band purified and sequenced as described above.

20 Polynucleotide sequences for the atpG, guAB, pnp, purF, and yjgF genes are set out in SEQ ID NOS: 166, 168, 170, 172 and 174, respectively. Polypeptides encoded by these genes are set out in SEQ ID NOS: 167, 169, 171, 173, and 175, respectively.

Numerous modifications and variations in the invention as set forth in the above illustrative examples are expected to occur to those skilled in the art. Consequently only such limitations as appear in the appended claims should be placed on the invention.

WHAT IS CLAIMED IS:

1. A gram-negative bacteria comprising a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 21, 25, 27, 29, 39, 41, 51, 53, 55, 57, 58, 60, 68, 72, 74, 76, 78, 80, 82, 84, 104, 108, 112, 116, 118, 120 122, 124, 126, 128, and 130, or species homologs thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.
2. The gram-negative bacteria of claim 1 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.
3. The gram-negative bacteria of claim 1 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.
4. The gram-negative bacteria of claim 1 wherein said mutation results in deletion of all or part of said gene.
5. An attenuated *Pasteurellaceae* bacteria comprising a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172 and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.
6. The *Pasteurellaceae* bacteria of claim 5 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.
7. The *Pasteurellaceae* bacteria of claim 5 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

8. The *Pasteurellaceae* bacteria of claim 5 wherein said mutation results in deletion of all or part of said gene.

9. The *Pasteurellaceae* bacteria of claim 5 selected from the group consisting of *Pasteurella (Mannheimia) haemolytica*, *Pasteurella multocida*, *Actinobacillus pleuropneumoniae* and *Haemophilus somnus*.

10. The *Pasteurellaceae* bacteria of claim 9 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

11. The *Pasteurellaceae* bacteria of claim 9 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

12. The *Pasteurellaceae* bacteria of claim 9 wherein said mutation results in deletion of all or part of said gene.

13. The attenuated *Pasteurellaceae* bacteria of claim 9 that is a *P. multocida* bacteria.

14. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

15. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

16. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in deletion of all or part of said gene.

17. The attenuated *Pasteurellaceae* bacteria of claim 9 that is a *A. pleuropneumoniae* bacteria.

18. The *Pasteurellaceae* bacteria of claim 17 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

19. The *Pasteurellaceae* bacteria of claim 17 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

20. The *Pasteurellaceae* bacteria of claim 17 wherein said mutation results in deletion of all or part of said gene.

21. An immunogenic composition comprising the bacteria according to any one of claims 1 through 20.

22. A vaccine composition comprising the immunogenic composition according to claim 21 and a pharmaceutically acceptable carrier.

23. The vaccine composition according to claim 22 further comprising an adjuvant.

24. A method for producing a gram-negative bacteria mutant comprising the step of introducing a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

25. A method for producing an attenuated *Pasteurellaceae* bacteria comprising the step of introducing a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29,

31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

26. A purified and isolated *Pasteurellaceae* polynucleotide comprising a nucleotide sequence selected from the group consisting of nucleotide sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172 and 174.

27. A purified and isolated *Pasteurellaceae* polynucleotide comprising a nucleotide sequence selected from the group consisting of nucleotide sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 21, 25, 27, 29, 39, 41, 51, 53, 55, 57, 58, 60, 68, 72, 74, 76, 78, 80, 82, 84, 104, 108, 112, 116, 118, 120, 122, 124, 126, 128, and 130.

28. A purified and isolated polynucleotide encoding a *Pasteurellaceae* virulence gene product, or species homolog thereof, selected from the group consisting of:

- the polynucleotide according to claim 27,
- polynucleotides encoding a polypeptide encoded by the polynucleotide of (a), and
- polynucleotides that hybridize to the complement of the polynucleotides of (a) or (b) under moderate stringency conditions.

29. A purified and isolated *Pasteurellaceae* polynucleotide encoding a polypeptide selected from the group consisting of polypeptides having amino acid sequences set forth in SEQ ID NOs: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109,

111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 165, 167, 169, 171, 173, and 175.

30. The polynucleotide of claim 29 which is a DNA.

31. A vector comprising the DNA of claim 30.

32. The vector of claim 31 that is an expression vector, wherein the DNA is operatively linked to an expression control DNA sequence.

33. A host cell stably transformed or transfected with the DNA of claim 30 in a manner allowing the expression of the encoded polypeptide in said host cell.

34. A method for producing a recombinant polypeptide comprising culturing the host cell of claim 33 in a nutrient medium and isolating the encoded polypeptide from said host cell or said nutrient medium.

35. A purified polypeptide produced by the method of claim 34.

36. A purified polypeptide comprising a polypeptide selected from the group consisting of polypeptides having amino acid sequences set forth in SEQ ID NOs: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 165, 167, 169, 171, 173, and 175.

37. An antibody that is specifically reactive with the polypeptide of claim 36.

38. The antibody of claim 33 that is a monoclonal antibody.

39. A method of using the monoclonal antibody of claim 39 for identifying a bacteria of claim 1, 5, 9, or 13 comprising the step of contacting an extract of bacteria with said monoclonal antibody and detecting the absence of binding of said monoclonal antibody.

40. A method of identifying an anti-bacterial agent comprising the steps of assaying potential agents for the ability to interfere with expression or activity of gene products represented by the amino acid sequences set forth in any one of SEQ ID NOS: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 165, 167, 169, 171, 173, and 175 and identifying an agent that interferes with expression or activity of said gene products.

41. A method of identifying an anti-bacterial agent comprising the steps of:

- a) measuring expression or activity of a gene product as set out in SEQ ID NOS: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 165, 167, 169, 171, 173, and 175;
- b) contacting the gene product in (a) with a test compound
- c) measuring expression or activity of the gene product in the presence of the test compound; and
- d) identifying the test compound as an antibacterial agent when expression or activity of the gene product is decreased in the presence of the test compound as compared to expression or activity in the presence of the test compound.

SEQUENCE LISTING

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gtg cct agc aag atg caa tgt ttt gag ata atg gtt gat tgg att Val Pro Ser Lys Met Gln Cys Phe Val Glu Ile Met Val Asp Trp Ile 60	65		70	425
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ggc tta tca att ggt gtc ttc ttc tta att att ttc tat aca atc aaa Gly Leu Ser Ile Gly Val Phe Phe Leu Ile Ile Phe Tyr Thr Ile Lys 140	145		150	665
tca aaa ggt atg agt ggc ttt gtt aaa gaa tat acg ctt cat cct ttt Ser Lys Gly Met Ser Gly Phe Val Lys Glu Tyr Thr Leu His Pro Phe 155	160		165	713
aat cat cct ttg tta att ccg gtt aac tta gcg ctt gaa tca gtc aca Asn His Pro Leu Leu Ile Pro Val Asn Leu Ala Leu Glu Ser Val Thr 170	175		180	761
tta tta gca aaa cct gtt tct ttg gcg ttc cgt ctt ttc ggg aat atg Leu Leu Ala Lys Pro Val Ser Leu Ala Phe Arg Leu Phe Gly Asn Met 185	190	195	200	809
tat gca ggt gaa ctt atc ttt att ctt att gca gtg atg tac atg gca Tyr Ala Gly Glu Leu Ile Phe Ile Leu Ile Ala Val Met Tyr Met Ala 205	210		215	857
aat aat ttt gca ctt aat tca atg ggt att ttc atg cat ttg gct tgg Asn Asn Phe Ala Leu Asn Ser Met Gly Ile Phe Met His Leu Ala Trp 220	225		230	905
gct att ttc cat att ctt gtg att acc tta caa gca ttt att ttt atg Ala Ile Phe His Ile Leu Val Ile Thr Leu Gln Ala Phe Ile Phe Met 235	240		245	953
atg ctt aca gtg gtt tat ttg agt atg ggt tat aac aaa gca gaa cac Met Leu Thr Val Val Tyr Leu Ser Met Gly Tyr Asn Lys Ala Glu His 250	255		260	1001
taattttta taaaacaaaac cagacccttgg gtctaaattt caatcttatg gagaacatta	1061			
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<213> Pasteurella multocida

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Val Ala Lys Lys Ala Thr Pro Gly Val Pro Ser Lys Met Gln Cys Phe
50 55 60
Val Glu Ile Met Val Asp Trp Ile Asp Gly Ile Val Lys Glu Asn Phe
65 70 75 80
His Gly Pro Arg His Ala Val Gly Pro Leu Ala Leu Thr Ile Phe Cys
85 90 95
Trp Val Phe Ile Met Asn Ala Ile Asp Leu Ile Pro Val Asp Phe Leu
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Pro Gln Leu Ala His Leu Phe Gly Ile Glu Tyr Leu Arg Ala Val Pro
115 120 125
Thr Ala Asp Ile Ser Gly Thr Leu Gly Leu Ser Ile Gly Val Phe Phe
130 135 140
Leu Ile Ile Phe Tyr Thr Ile Lys Ser Lys Gly Met Ser Gly Phe Val
145 150 155 160
Lys Glu Tyr Thr Leu His Pro Phe Asn His Pro Leu Leu Ile Pro Val
165 170 175
Asn Leu Ala Leu Glu Ser Val Thr Leu Leu Ala Lys Pro Val Ser Leu
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Ala Phe Arg Leu Phe Gly Asn Met Tyr Ala Gly Glu Leu Ile Phe Ile
195 200 205
Leu Ile Ala Val Met Tyr Met Ala Asn Asn Phe Ala Leu Asn Ser Met
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Gly Ile Phe Met His Leu Ala Trp Ala Ile Phe His Ile Leu Val Ile
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<213> Pasteurella multocida

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tatgcgtgag ttaacccaat ctggcaatta caatgtatgaa attaaagagt cattaaaagg 300
cattttggat agcttcaaaag caaacatgtgc gtggtaagtt aacactttaa atggagagac 360
aaa atg gca ggt gct aaa gag ata aga acc aaa atc gcg agt gta aaa 408
Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys
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agt aca caa aaa att act aaa gcg atg gaa atg gtt gct gcc tcg aaa 456
Ser Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys
    20          25           30

atg cgt aaa acg caa gaa cgc atg tct tct tca cgc cct tat tca gaa 504
Met Arg Lys Thr Gln Glu Arg Met Ser Ser Ser Arg Pro Tyr Ser Glu
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aca ata cgt aac gtg att agc cac gtt tcc aaa gca acg att ggt tac 552
Thr Ile Arg Asn Val Ile Ser His Val Ser Lys Ala Thr Ile Gly Tyr
    50          55           60

aag cat cca ttt tta gtg gat cgc gaa gta aaa aaa gtg ggc atg att 600
Lys His Pro Phe Leu Val Asp Arg Glu Val Lys Lys Val Gly Met Ile
    65          70           75

gtt gtg tcc aca gat cgt ggt ctt tgt ggt ggc tta aac gtg aac ttg 648
Val Val Ser Thr Asp Arg Gly Leu Cys Gly Leu Asn Val Asn Leu
    80          85           90           95

ttt aaa act gta tta aat gaa atg aaa gaa tgg aaa gaa aaa gat gtt 696
Phe Lys Thr Val Leu Asn Glu Met Lys Glu Trp Lys Glu Lys Asp Val
    100         105          110

tcc gtt caa ttg agt tta atc ggt tct aaa tct atc aac ttt ttc caa 744
Ser Val Gln Leu Ser Leu Ile Gly Ser Lys Ser Ile Asn Phe Phe Gln
    115         120          125

tct ttg gga att aaa att tta acc caa gat tca ggt att ggt gat act 792
Ser Leu Gly Ile Lys Ile Leu Thr Gln Asp Ser Gly Ile Gly Asp Thr
    130         135          140

ccc tct gtt gag cag tta att ggt tca gtc aat tct atg att gat gct 840
Pro Ser Val Glu Gln Leu Ile Gly Ser Val Asn Ser Met Ile Asp Ala
    145         150          155

tat aaa aaa ggg gaa gta gat gtt gtg tat tta gtt tat aac aaa ttt 888
Tyr Lys Lys Gly Glu Val Asp Val Val Tyr Leu Val Tyr Asn Lys Phe
    160         165          170          175

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att aac acg atg tcg caa aag cca gta ttg gaa aaa tta att cca tta Ile Asn Thr Met Ser Gln Lys Pro Val Leu Glu Lys Leu Ile Pro Leu 180 185 190	936
cca gaa tta gat aat gat gaa tta ggc gaa aga aaa caa gtt tgg gat Pro Glu Leu Asp Asn Asp Glu Leu Gly Glu Arg Lys Gln Val Trp Asp 195 200 205	984
tat att tac gaa cct gat gcg aaa gta tta gat aat tta ttg gtt Tyr Ile Tyr Glu Pro Asp Ala Lys Val Leu Leu Asp Asn Leu Leu Val 210 215 220	1032
cgt tat tta gaa tct cag gtt tat caa gca gca gtt gaa aac ctt gct Arg Tyr Leu Glu Ser Gln Val Tyr Gln Ala Ala Val Glu Asn Leu Ala 225 230 235	1080
tct gag caa gcc gct cga atg gtc gcc atg aaa gca gca aca gat aac Ser Glu Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn 240 245 250 255	1128
gca ggt aac tta att aat gag tta cag tta gtc tat aac aaa gct cgt Ala Gly Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg 260 265 270	1176
caa gca agt att aca aat gaa tta aat gaa att gtt gcc ggt gca gca Gln Ala Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala 275 280 285	1224
gca att taacaaatag aggatcggtta atggcaactg gaaaaattgt acaaatcatc Ala Ile	1280
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<213> Pasteurella multocida

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35	40	45	
Ile Arg Asn Val Ile Ser His Val Ser Lys Ala Thr Ile Gly Tyr Lys			
50	55	60	
His Pro Phe Leu Val Asp Arg Glu Val Lys Lys Val Gly Met Ile Val			
65	70	75	80
Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Val Asn Leu Phe			
85	90	95	
Lys Thr Val Leu Asn Glu Met Lys Glu Trp Lys Glu Lys Asp Val Ser			
100	105	110	
Val Gln Leu Ser Leu Ile Gly Ser Lys Ser Ile Asn Phe Phe Gln Ser			
115	120	125	
Leu Gly Ile Lys Ile Leu Thr Gln Asp Ser Gly Ile Gly Asp Thr Pro			
130	135	140	
Ser Val Glu Gln Leu Ile Gly Ser Val Asn Ser Met Ile Asp Ala Tyr			
145	150	155	160
Lys Lys Gly Glu Val Asp Val Val Tyr Leu Val Tyr Asn Lys Phe Ile			
165	170	175	
Asn Thr Met Ser Gln Lys Pro Val Leu Glu Lys Leu Ile Pro Leu Pro			
180	185	190	
Glu Leu Asp Asn Asp Glu Leu Gly Glu Arg Lys Gln Val Trp Asp Tyr			
195	200	205	
Ile Tyr Glu Pro Asp Ala Lys Val Leu Leu Asp Asn Leu Leu Val Arg			
210	215	220	
Tyr Leu Glu Ser Gln Val Tyr Gln Ala Ala Val Glu Asn Leu Ala Ser			
225	230	235	240
Glu Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala			
245	250	255	
Gly Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln			
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Ile			

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 Glu Phe Tyr Pro Leu Glu Ala Val Lys Thr Asn Ile Leu Gly Thr Ala
 20 25 30

aat gtc tta gaa gcc gcc atc caa aac cag ata aaa cgc gtc gtc tgt 144
 Asn Val Leu Glu Ala Ala Ile Gln Asn Gln Ile Lys Arg Val Val Cys
 35 40 45

ctt agc aca gat aaa gcg gtg tac cca att aat gcg atg ggc att tct 192
 Leu Ser Thr Asp Lys Ala Val Tyr Pro Ile Asn Ala Met Gly Ile Ser
 50 55 60

aaa gca atg atg gaa aaa gtc atc atc gca aaa tcg cgt aac cta gaa 240
 Lys Ala Met Met Glu Lys Val Ile Ile Ala Lys Ser Arg Asn Leu Glu
 65 70 75 80

ggc aca cca acg aca atc tgt tgt act cgc tat ggc aat gtc atg gca 288
 Gly Thr Pro Thr Ile Cys Cys Thr Arg Tyr Gly Asn Val Met Ala
 85 90 95

tcg cgt ggt tcg gtt atc cca tta ttt gtc gat caa ata cgt caa ggc 336
 Ser Arg Gly Ser Val Ile Pro Leu Phe Val Asp Gln Ile Arg Gln Gly
 100 105 110

aag cct ttt act att act gat cct gag atg aca cgc ttt atg atg aca 384
 Lys Pro Phe Thr Ile Thr Asp Pro Glu Met Thr Arg Phe Met Met Thr
 115 120 125

ttg gaa gat gct gtg gat tta gtc cta tat gca ttt aaa aat ggt caa 432
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 130 135 140

aat ggt gat gtt ttt gta caa aaa gcc ccc gca gca acc att ggt acc 480
 Asn Gly Asp Val Phe Val Gln Lys Ala Pro Ala Ala Thr Ile Gly Thr
 145 150 155 160

ctt gcc aaa gca att acc gaa tta tta tct gtc cca aat cac cct att 528
 Leu Ala Lys Ala Ile Thr Glu Leu Ser Val Pro Asn His Pro Ile
 165 170 175

tcc att ata ggt acg cgt cat gga gag aaa gca ttc gaa gct tta tta 576
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 180 185 190

agc cgt gaa gaa atg gtt cat gca att aat gaa ggt aat tat tat cgc 624
 Ser Arg Glu Glu Met Val His Ala Ile Asn Glu Gly Asn Tyr Tyr Arg
 195 200 205

atc cca gcc gat caa cgc agt tta aat tac agt aaa tat gtc gaa aaa 672
 Ile Pro Ala Asp Gln Arg Ser Leu Asn Tyr Ser Lys Tyr Val Glu Lys
 210 215 220

ggg gaa cca aaa att acc gaa gtc acc gac tac aac tca cat aat act		720
Gly Glu Pro Lys Ile Thr Glu Val Thr Asp Tyr Asn Ser His Asn Thr		
225	230	235
235		240
gag cgt ttg act gtc aag gaa atg aag cag tta ctg ctt aaa ctt gaa		768
Glu Arg Leu Thr Val Lys Glu Met Lys Gln Leu Leu Lys Leu Glu		
245	250	255
ttc ata cag aaa atg att gag ggt gaa tac atc tca ccg gag gta		813
Phe Ile Gln Lys Met Ile Glu Gly Glu Tyr Ile Ser Pro Glu Val		
260	265	270
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Asn Val Leu Glu Ala Ala Ile Gln Asn Gln Ile Lys Arg Val Val Cys			
35	40	45	
Leu Ser Thr Asp Lys Ala Val Tyr Pro Ile Asn Ala Met Gly Ile Ser			
50	55	60	
Lys Ala Met Met Glu Lys Val Ile Ile Ala Lys Ser Arg Asn Leu Glu			
65	70	75	80
Gly Thr Pro Thr Thr Ile Cys Cys Thr Arg Tyr Gly Asn Val Met Ala			
85	90	95	
Ser Arg Gly Ser Val Ile Pro Leu Phe Val Asp Gln Ile Arg Gln Gly			
100	105	110	
Lys Pro Phe Thr Ile Thr Asp Pro Glu Met Thr Arg Phe Met Met Thr			
115	120	125	

Leu Glu Asp Ala Val Asp Leu Val Leu Tyr Ala Phe Lys Asn Gly Gln
 130 135 140
 Asn Gly Asp Val Phe Val Gln Lys Ala Pro Ala Ala Thr Ile Gly Thr
 145 150 155 160
 Leu Ala Lys Ala Ile Thr Glu Leu Leu Ser Val Pro Asn His Pro Ile
 165 170 175
 Ser Ile Ile Gly Thr Arg His Gly Glu Lys Ala Phe Glu Ala Leu Leu
 180 185 190
 Ser Arg Glu Glu Met Val His Ala Ile Asn Glu Gly Asn Tyr Tyr Arg
 195 200 205
 Ile Pro Ala Asp Gln Arg Ser Leu Asn Tyr Ser Lys Tyr Val Glu Lys
 210 215 220
 Gly Glu Pro Lys Ile Thr Glu Val Thr Asp Tyr Asn Ser His Asn Thr
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 Glu Arg Leu Thr Val Lys Glu Met Lys Gln Leu Leu Leu Lys Leu Glu
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 Met Asn Thr Ile Ile Phe Asp Ser Ala Gln His Ala Val
 1 5 10

 gag aaa att gca caa gaa ttg tta gcg tat agc tta gaa ggt cgc cct 4118
 Glu Lys Ile Ala Gln Glu Leu Leu Ala Tyr Ser Ile Glu Gly Arg Pro
 15 20 25

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 30 35 40 45

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 Thr Leu Ala Gln Ala Pro Tyr Asn Thr Glu Ile Gln Trp Lys Asn Leu
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His Phe Trp Trp Gly Asp Asp Arg Met Val Pro Pro Thr Asp Pro Glu			
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cct gca gaa aat att cac cgc att cgt ggt gaa gcc ccc gtt gag agt			4358
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Glu Leu His Arg Phe Glu Gln Ala Leu Ser Ala Val Ile Pro Gly Gln			
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Val Phe Asp Trp Ile Ile Leu Gly Met Gly Thr Asp Gly His Thr Ala			
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Ser Leu Phe Pro His Gln Thr Asp Phe Asp Asp Pro His Phe Ala Val			
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Ile Ala Lys His Pro Glu Thr Gly Gln Ile Arg Ile Ser Lys Thr Ala			
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Lys Leu Ile Glu Gln Ala Lys Arg Val Thr Tyr Leu Val Thr Gly Ser			
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Ser Lys Ala Glu Ile Leu Lys Glu Ile Gln Thr Thr Pro Ala Glu Gln			
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Gln Ala Pro Tyr Asn Thr Glu Ile Gln Trp Lys Asn Leu His Phe Trp
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Gly Glu Val Gln Lys Leu Leu Phe Asp His Ile Gln Ile Pro Ala Glu
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Asn Ile His Arg Ile Arg Gly Glu Ala Pro Val Glu Ser Glu Leu His
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Arg Phe Glu Gln Ala Leu Ser Ala Val Ile Pro Gly Gln Val Phe Asp
115 120 125
Trp Ile Ile Leu Gly Met Gly Thr Asp Gly His Thr Ala Ser Leu Phe
130 135 140
Pro His Gln Thr Asp Phe Asp Asp Pro His Phe Ala Val Ile Ala Lys

145	150	155	160
His Pro Glu Thr Gly Gln Ile Arg Ile Ser Lys Thr Ala Lys Leu Ile			
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Ser Arg Leu Arg Trp Gly Glu Ser Tyr Gln Leu Val Pro Leu Asn Asp			
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Gln Gln Lys Ile His Val Leu Gln Lys Asn Ala His Gln Arg Gly Ile			
190	195	200	
gaa ctc ccc gat gaa gta gct aat ttt ctt ttg aaa cgc tta gag cgc			2294
Glu Leu Pro Asp Glu Val Ala Asn Phe Leu Leu Lys Arg Leu Glu Arg			
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Asp Met Lys Thr Leu Phe Glu Ala Leu Ser Lys Leu Asp Lys Ala Ser			
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His Gln Leu Asp Asp Glu Thr Leu Asp Asn Phe Tyr Pro Asp Asn Asn			
35	40	45	
Leu Leu Leu Leu Asn Ser Leu Arg Lys Asn Phe Thr Cys Leu Thr Gln			
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Gln Phe Phe Tyr Ile Trp Gly Glu Gln Ser Ser Gly Lys Ser His Leu			
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Leu Lys Gly Ile Thr His His Phe Phe Leu Leu Gln Arg Pro Ala Ile			
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Tyr Val Pro Leu Glu Lys Ser Gln Tyr Phe Ser Pro Ala Val Leu Glu			
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Asn Leu Glu Gln Gln Leu Val Cys Leu Asp Asn Leu Gln Ala Ile			
115	120	125	
Ile Gly Asn Thr Glu Trp Glu Leu Ala Ile Phe Asp Leu Phe Asn Arg			
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145	150	155	160

Pro Thr Ala Leu Pro Val Ser Leu Pro Asp Leu Ala Ser Arg Leu Arg
165 170 175

Trp Gly Glu Ser Tyr Gln Leu Val Pro Leu Asn Asp Gln Gln Lys Ile
180 185 190

His Val Leu Gln Lys Asn Ala His Gln Arg Gly Ile Glu Leu Pro Asp
195 200 205

Glu Val Ala Asn Phe Leu Leu Lys Arg Leu Glu Arg Asp Met Lys Thr
210 215 220

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Met Leu Ser Phe Phe Lys Thr Leu Ser Thr Lys Arg

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35 40 45

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65 70 75 80

Ser Ala Ile Lys Gly Leu Met Ile Ser Ile Thr His Leu Asp Leu Gln
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Leu Tyr Pro Ala Pro Trp Lys Gln Cys Ser Ala Val Ala Glu Phe Pro
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115 120 125

Gly Ser Cys Ser Glu Val Thr Trp Gln Phe Leu Gly Phe Ser Met Val
130 135 140

Gln Trp Ile Val Val Ile Phe Ala Leu Tyr Thr Leu Leu Ala Leu
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Glu Arg Phe Leu Phe Leu Ser Arg Val Asn Val Ala Ser Tyr Glu Ser
35 40 45

Ile His Glu Leu Asp Ile Asp Leu Gln Arg His Leu Thr Ala Ile Ser
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Thr Ile Gly Ser Asn Ala Pro Tyr Val Gly Leu Leu Gly Thr Val Ile

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Asp Ala Ala Ala Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr			
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Ala Val Gly Ile Leu Val Ala Ile Pro Ala Met Val Cys Tyr Asn Gly			
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 Glu Asn Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu
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 Arg Ser Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr
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 Asn Phe Ser Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met																																																																																																																					
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 Tyr Gln Lys Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys																																																																																																																					
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 Ser Tyr Asp Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro																																																																																																																					
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 Lys Leu Glu Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu
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 Val Gly Asp Lys Asn Ala Asp Met Arg Arg His Asn Ala Ala Gly Thr
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 1860 1865 1870
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 1890 1895 1900
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 1905 1910 1915 1920
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 1940 1945 1950

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 1955 1960 1965
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 1970 1975 1980
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 2005 2010 2015
 Gly Lys Thr Ala Ala Ser Val Lys Trp Gln Val Pro Val Ala Val Ala
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 gatcttgaat ttattgtact gtggggaga actcgcgatc tgtttgaa tggggagaaaa 240
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 ggtgtgagtg gtgttacgca acatcgtcaa aaaccgattt attatttctc aggatcactt 1440
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 Met Asn Lys Asn Arg Tyr
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Lys Leu Ile Phe Ser Gln Val Lys Gly Cys Leu Val Pro Val Ala Glu	
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tgt att aac tca gct att agc aat ggt tca tct gat tca aca tcc aca	1592
Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser Ser Asp Ser Thr Ser Thr	
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Ser Glu Gln Val Glu Glu Pro Phe Leu Leu Glu Gln Tyr Ser Leu	
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gca atg caa ttg act tgg aaa cag ctt tct att tta ttt tta act gtg	1736
Ala Met Gln Leu Thr Trp Lys Gln Leu Ser Ile Leu Phe Leu Thr Val	
75 80 85	
att tct gtt cct gtt ttg gct gag gga aaa ggg gat gaa aga aat caa	1784
Ile Ser Val Pro Val Leu Ala Glu Gly Lys Gly Asp Glu Arg Asn Gln	
90 95 100	
tta aca gtg att gat aat agc gat cat att aaa tta gat gca tct aat	1832
Leu Thr Val Ile Asp Asn Ser Asp His Ile Lys Leu Asp Ala Ser Asn	
105 110 115	
ctt gct ggt aat gat aaa aca aaa atc tat caa gca gaa aat aaa gtt	1880
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 Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser
 145 150 155 160
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 Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala
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 Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val
 195 200 205
 Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn
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 225 230 235 240
 Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu
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Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn
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 385 390 395 400
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 405 410 415
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 420 425 430
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 465 470 475 480
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 485 490 495
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 Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg
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 Val Asp Leu Ala Gly Glu Lys Val Ser Leu Asn Phe Gly Asp Ile Ile
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cat gct tac caa aac cag ccc cta tca aca aaa gtt gtt ttt caa tta His Ala Tyr Gln Asn Gln Pro Leu Ser Thr Lys Val Val Phe Gln Leu	96
20 25 30	
gtg aaa gat ttg acg gaa gtt tta tac cgt tct ggc tac gtg aca agt Val Lys Asp Leu Thr Glu Val Leu Tyr Arg Ser Gly Tyr Val Thr Ser	144
35 40 45	
gca att ggt tta aaa aat tca aaa atc agc aat ggc gat ctt gaa ttt Ala Ile Gly Leu Lys Asn Ser Lys Ile Ser Asn Gly Asp Leu Glu Phe	192
50 55 60	
att gta ctg tgg gga aga act cgc gat ctg ttt gtg aat ggg gag aaa Ile Val Leu Trp Gly Arg Thr Arg Asp Leu Phe Val Asn Gly Glu Lys	240
65 70 75 80	
cca acc cgt ttt aga gat aaa aca atg tta tca gtc cta ccc aat tta Pro Thr Arg Phe Arg Asp Lys Thr Met Leu Ser Val Leu Pro Asn Leu	288
85 90 95	
atc gga aat cgc tta agt att cac gac att gac cag ttg atc gaa atc Ile Gly Asn Arg Leu Ser Ile His Asp Ile Asp Gln Leu Ile Glu Ile	336
100 105 110	
tta aat act acg aat aaa aaa gcc aca gtg aat gtg gtt gca agt gaa Leu Asn Thr Asn Lys Lys Ala Thr Val Asn Val Ala Ser Glu	384
115 120 125	
† gaa aaa ggc agc tca aat cta aat att gaa aga caa tat gat gtt ttt Glu Lys Gly Ser Ser Asn Leu Asn Ile Glu Arg Gln Tyr Asp Val Phe	432
130 135 140	
ccg caa gtg agt gtc gga ttc aat aat tca ggt gct ggc aat aat gcc Pro Gln Val Ser Val Gly Phe Asn Asn Ser Gly Ala Gly Asn Asn Ala	480
145 150 155 160	
aat ggg cgt aat caa gct aca ttg aat att gct tgg agt gat cta tta Asn Gly Arg Asn Gln Ala Thr Leu Asn Ile Ala Trp Ser Asp Leu Leu	528
165 170 175	
ggc acg aat gat cgt tgg agt ttc tcg agt agt tac cgt tta tat aaa Gly Thr Asn Asp Arg Trp Ser Phe Ser Ser Ser Tyr Arg Leu Tyr Lys	576
180 185 190	
aat cat cat gct aac cag caa cgc aat tat act ttg tct tac agt cag Asn His His Ala Asn Gln Gln Arg Asn Tyr Thr Leu Ser Tyr Ser Gln	624
195 200 205	
cct ata ggc ttt tct aca gta gaa att aaa gca tcg gaa tct acg tat Pro Ile Gly Phe Ser Thr Val Glu Ile Lys Ala Ser Glu Ser Thr Tyr	672
210 215 220	
gaa aaa gaa ctt cgc ggt ata aat act cat tct tct cat ggg aaa acc Glu Lys Glu Leu Arg Gly Ile Asn Thr His Ser Ser His Gly Lys Thr	720
225 230 235 240	
caa agc tta gct gtc aag ctg atg cat gtg tta ttg cgt aat aag gag Gln Ser Leu Ala Val Lys Leu Met His Val Leu Leu Arg Asn Lys Glu	768
245 250 255	
agt att tta tct aca tat acc gag ttc gag ttt aaa aaa cgg att agt Ser Ile Leu Ser Thr Tyr Thr Glu Phe Glu Phe Lys Lys Arg Ile Ser	816
260 265 270	

tat ttt tct gat att ttg att ggg aaa tat cac aat aat aaa gtg agc Tyr Phe Ser Asp Ile Leu Ile Gly Lys Tyr His Asn Asn Lys Val Ser 275 280 285	864
gta ggg tta tct tac atg act aat ttt gct tac ggg aag ctt tac agc Val Gly Leu Ser Tyr Met Thr Asn Phe Ala Tyr Gly Lys Leu Tyr Ser 290 295 300	912
gac att gct tac gcg aat ggg ttg aga tgg ttt ggg gcg aat tat tca Asp Ile Ala Tyr Ala Asn Gly Leu Arg Trp Phe Gly Ala Asn Tyr Ser 305 310 315 320	960
gca tat gat gca aat cgt gaa aaa acc tta aaa tta ttg tca gga agt Ala Tyr Asp Ala Asn Arg Glu Lys Thr Leu Lys Leu Ser Gly Ser 325 330 335	1008
att aat tgg cag cgt cca ata tcc ctg ttt gaa cgt gcg atg aat tat Ile Asn Trp Gln Arg Pro Ile Ser Leu Phe Glu Arg Ala Met Asn Tyr 340 345 350	1056
caa tta cgt att ggt gcc caa tat ggt ttt gat agt ttg tat tct gaa Gln Leu Arg Ile Gly Ala Gln Tyr Gly Phe Asp Ser Leu Tyr Ser Glu 355 360 365	1104
aat caa ttt tca att ggt gat gaa tat aca gta aga gga ttt aaa ggt Asn Gln Phe Ser Ile Gly Asp Glu Tyr Thr Val Arg Gly Phe Lys Gly 370 375 380	1152
ggg gcg gtt tct ggt gat agt ggt gcg tat tta tca caa aca ctg acg Gly Ala Val Ser Gly Asp Ser Gly Ala Tyr Leu Ser Gln Thr Leu Thr 385 390 395 400	1200
gtt cct ttt tat cca caa aaa gca tat tta tct cag gta tcc cct ttt Val Pro Phe Tyr Pro Gln Lys Ala Tyr Leu Ser Gln Val Ser Pro Phe 405 410 415	1248
att gga ttt gat atg ggt aaa gta cat att aaa tca aag cat aaa aca Ile Gly Phe Asp Met Gly Lys Val His Ile Lys Ser Lys His Lys Thr 420 425 430	1296
acc act tta gtc ggt ttt gcc cta ggc ttg aaa acg caa ata aag tta Thr Thr Leu Val Gly Phe Ala Leu Gly Leu Lys Thr Gln Ile Lys Leu 435 440 445	1344
ttt tca tta tca tta acc tat gca caa cca atg aat ggt gtg agt ggt Phe Ser Leu Ser Leu Thr Tyr Ala Gln Pro Met Asn Gly Val Ser Gly 450 455 460	1392
gtt acg caa cat cgt caa aaa ccg att tat tat ttc tca gga tca ctt Val Thr Gln His Arg Gln Lys Pro Ile Tyr Tyr Phe Ser Gly Ser Leu 465 470 475 480	1440
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aaactcattt ttagtcaagt caaagggttgt ctcgttcctg tggcagaatg tattaaactca	1556
gctattagca atggttcatc tgattcaaca tccacatcg aacaaggtaa agaggaacct	1616
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<210> 20
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<212> PRT
<213> Pasteurella multocida

<400> 20
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His Ala Tyr Gln Asn Gln Pro Leu Ser Thr Lys Val Val Phe Gln Leu
 20 25 30

Val Lys Asp Leu Thr Glu Val Leu Tyr Arg Ser Gly Tyr Val Thr Ser
 35 40 45

Ala Ile Gly Leu Lys Asn Ser Lys Ile Ser Asn Gly Asp Leu Glu Phe
 50 55 60

Ile Val Leu Trp Gly Arg Thr Arg Asp Leu Phe Val Asn Gly Glu Lys
 65 70 75 80

Pro Thr Arg Phe Arg Asp Lys Thr Met Leu Ser Val Leu Pro Asn Leu
 85 90 95

Ile Gly Asn Arg Leu Ser Ile His Asp Ile Asp Gln Leu Ile Glu Ile
 100 105 110

Leu Asn Thr Thr Asn Lys Lys Ala Thr Val Asn Val Val Ala Ser Glu
 115 120 125

Glu Lys Gly Ser Ser Asn Leu Asn Ile Glu Arg Gln Tyr Asp Val Phe
 130 135 140

Pro Gln Val Ser Val Gly Phe Asn Asn Ser Gly Ala Gly Asn Asn Ala
 145 150 155 160

Asn Gly Arg Asn Gln Ala Thr Leu Asn Ile Ala Trp Ser Asp Leu Leu
 165 170 175

Gly Thr Asn Asp Arg Trp Ser Phe Ser Ser Ser Tyr Arg Leu Tyr Lys
 180 185 190

Asn His His Ala Asn Gln Gln Arg Asn Tyr Thr Leu Ser Tyr Ser Gln
 195 200 205

Pro Ile Gly Phe Ser Thr Val Glu Ile Lys Ala Ser Glu Ser Thr Tyr
 210 215 220

Glu Lys Glu Leu Arg Gly Ile Asn Thr His Ser Ser His Gly Lys Thr
 225 230 235 240

Gln Ser Leu Ala Val Lys Leu Met His Val Leu Leu Arg Asn Lys Glu
 245 250 255

Ser Ile Leu Ser Thr Tyr Thr Glu Phe Glu Phe Lys Lys Arg Ile Ser
 260 265 270

Tyr Phe Ser Asp Ile Leu Ile Gly Lys Tyr His Asn Asn Lys Val Ser
 275 280 285

Val Gly Leu Ser Tyr Met Thr Asn Phe Ala Tyr Gly Lys Leu Tyr Ser
 290 295 300

Asp Ile Ala Tyr Ala Asn Gly Leu Arg Trp Phe Gly Ala Asn Tyr Ser
 305 310 315 320

Ala Tyr Asp Ala Asn Arg Glu Lys Thr Leu Lys Leu Leu Ser Gly Ser
 325 330 335

Ile Asn Trp Gln Arg Pro Ile Ser Leu Phe Glu Arg Ala Met Asn Tyr
 340 345 350

Gln Leu Arg Ile Gly Ala Gln Tyr Gly Phe Asp Ser Leu Tyr Ser Glu
 355 360 365
 Asn Gln Phe Ser Ile Gly Asp Glu Tyr Thr Val Arg Gly Phe Lys Gly
 370 375 380
 Gly Ala Val Ser Gly Asp Ser Gly Ala Tyr Leu Ser Gln Thr Leu Thr
 385 390 395 400
 Val Pro Phe Tyr Pro Gln Lys Ala Tyr Leu Ser Gln Val Ser Pro Phe
 405 410 415
 Ile Gly Phe Asp Met Gly Lys Val His Ile Lys Ser Lys His Lys Thr
 420 425 430
 Thr Thr Leu Val Gly Phe Ala Leu Gly Leu Lys Thr Gln Ile Lys Leu
 435 440 445
 Phe Ser Leu Ser Leu Thr Tyr Ala Gln Pro Met Asn Gly Val Ser Gly
 450 455 460
 Val Thr Gln His Arg Gln Lys Pro Ile Tyr Tyr Phe Ser Gly Ser Leu
 465 470 475 480
 Ser Phe

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<211> 1170
<212> DNA
<213> Pasteurella multocida

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<222> (639)..(1022)

<220>
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gtacgataag atcgccatgc atttcattgt ttttatTTT tccattgggt aatagactgg 180
tttcaaattt aattggtca cttagtagtacga gtttggcggt taaggcggtg agcacttttt 240
gtgtactggc gggtaacata aaggtactgg cttggtgccgc tacaatttt tcattacgt 300
ttaagttttt agccacaaaaa cctaggctgg tcccttcggg taaatgagcg ttgatttcag 360
caagatcaat ctcagcataa ctgaaatgac tgacgagtaa actacatata agtatcggtc 420
gtttgaaaag gcgtaaaaagc gtggcagtaa aaaaagaaga tattttatac ataattggct 480
cgagcagttt ctatTTTTT attgtcgaac aataatagta tttgaaccct cgagagtaaa 540
tccttttctc gttaaacact tatttttta ttcaactacg qcattgtttt tacaatgttq 600
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tggtttgtt tttatctaaa aaggaagaaa aaacgatt atg aaa cag att cca atg 656
 Met Lys Gln Ile Pro Met
 1 5

act ata cgt ggt gcg gaa caa tta aga caa gaa ctc gat ttt ttg aaa 704
 Thr Ile Arg Gly Ala Glu Gln Leu Arg Gln Glu Leu Asp Phe Leu Lys
 10 15 20

aac act cgt cgc cca gaa att att aat gct atc gca gaa gct cgt gaa 752
 Asn Thr Arg Arg Pro Glu Ile Ile Asn Ala Ile Ala Glu Ala Arg Glu
 25 30 35

cat ggc gat cta aaa gaa aat gca gaa tac cat gct gcg cgt gaa cag 800
 His Gly Asp Leu Lys Glu Asn Ala Glu Tyr His Ala Ala Arg Glu Gln
 40 45 50

caa gga ttt tgt gaa gga cga atc caa gaa att gaa ggg aaa tta gcg 848
 Gln Gly Phe Cys Glu Gly Arg Ile Gln Glu Ile Glu Gly Lys Leu Ala
 55 60 65 70

aat agt caa att att gat gtc aca aag atc cca aat aat ggc aaa gtg 896
 Asn Ser Gln Ile Ile Asp Val Thr Lys Ile Pro Asn Asn Gly Lys Val
 75 80 85

att ttt ggt gcc aca att ttg tta ctg aat att gac acg gaa gaa gaa 944
 Ile Phe Gly Ala Thr Ile Leu Leu Asn Ile Asp Thr Glu Glu Glu
 90 95 100

gtc tcg tac caa att gta ggc gat gat gaa gcc aat att aaa gca ggg 992
 Val Ser Tyr Gln Ile Val Gly Asp Asp Glu Ala Asn Ile Lys Ala Gly
 105 110 115

cta att tca gtt aac gcc acg cga ttg aat tagagaaagc taaatggatt 1042
 Leu Ile Ser Val Asn Ala Thr Arg Leu Asn
 120 125

gccaagatc ttggcgtcaa acaaacgtta attgacactt ccgtcattaa agcgattacg 1102
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 ttcggtga 1170

<210> 22
 <211> 128
 <212> PRT
 <213> Pasteurella multocida

<400> 22
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 1 5 10 15

Glu Leu Asp Phe Leu Lys Asn Thr Arg Arg Pro Glu Ile Ile Asn Ala
 20 25 30

Ile Ala Glu Ala Arg Glu His Gly Asp Leu Lys Glu Asn Ala Glu Tyr
 35 40 45

His Ala Ala Arg Glu Gln Gln Gly Phe Cys Glu Gly Arg Ile Gln Glu
 50 55 60

Ile Glu Gly Lys Leu Ala Asn Ser Gln Ile Ile Asp Val Thr Lys Ile
 65 70 75 80

Pro Asn Asn Gly Lys Val Ile Phe Gly Ala Thr Ile Leu Leu Leu Asn
 85 90 95

Ile Asp Thr Glu Glu Glu Val Ser Tyr Gln Ile Val Gly Asp Asp Glu
 100 105 110

Ala Asn Ile Lys Ala Gly Leu Ile Ser Val Asn Ala Thr Arg Leu Asn
 115 120 125

<210> 23

<211> 4666

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (980)..(2440)

<220>

<223> guaB

<400> 23

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 aatagcacat catttggcca ttttaatcca atgttcaaag cacctgcttg cttagcggtt 360
 tctgcgattt ccataccac tactaaactc aagccttcta aattgacattt ttggtcacat 420
 gccaataaca aactcataat cacttgcata gcaaaaggag aaagccattt acgaccacgt 480
 cgtccacgtc ccgcagttt atattctgtt aagcaaatag cgccttttc caaatgtgca 540
 atattgtcaa gcaagaattt attggtcgag ttaataatcg gcttaatata aagtgggtaa 600
 ggtgctaacg cttgcgtcaa ataagattca tttaaagcgac ttaatttggg tatgagacga 660
 aatgttggaa cttgctgttc tattttgttcc cttgttgtt tcaatttttc gatattgtgt 720
 aagatatctt gttctgaata acctaaaagt gcagtcaattt ctgctaaaga aagttgttga 780
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 aggcaactta ttatagacaa tgatttttc gaaaatcgat aaaaaaatcc atttcaaac 900
 agcaacgaaa tctgtataat ggcacccgaa tattttttac ctttttattt ttcatataaa 960
 cctaagagag aatattgca atg tta cga gta ata aaa gaa gca tta acc ttc 1012
 Met Leu Arg Val Ile Lys Glu Ala Leu Thr Phe
 1 5 10

gat gat gtt ttg ctt gtc cca gca cat tct act gtg ctc cca aat acc 1060
 Asp Asp Val Leu Leu Val Pro Ala His Ser Thr Val Leu Pro Asn Thr
 15 20 25

gca gac ctt tcc actcaa ctc acc aaa act atc cgc ctc aat atc cca Ala Asp Leu Ser Thr Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro 30 35 40	1108
atg tta tcc gcc gcc atg gat acc gtg aca gaa act aaa ctg gca atc Met Leu Ser Ala Ala Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile 45 50 55	1156
tct ctt gca caa gaa ggt ggc atc ggg ttt att cat aaa aat atg tct Ser Leu Ala Gln Glu Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser 60 65 70 75	1204
att gag cgt caa gcg gaa cgt gtc cgc aaa gtg aaa aaa ttt gag agc Ile Glu Arg Gln Ala Glu Arg Val Arg Lys Val Lys Lys Phe Glu Ser 80 85 90	1252
ggt att gta tcc gat cct gtc acc gtt tca cca acc tta tct tta gca Gly Ile Val Ser Asp Pro Val Thr Val Ser Pro Thr Leu Ser Leu Ala 95 100 105	1300
gaa tta agt gaa tta gtg aag aaa aat ggt ttt gcg agt ttc cct gtt Glu Leu Ser Glu Leu Val Lys Lys Asn Gly Phe Ala Ser Phe Pro Val 110 115 120	1348
gtt gat gat gaa aaa aat ctt gtc ggt atc att act ggt cgt gat aca Val Asp Asp Glu Lys Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr 125 130 135	1396
cgc ttt gtc acg gat tta aat aaa aca gtg gcg gac ttt atg acc cct Arg Phe Val Thr Asp Leu Asn Lys Thr Val Ala Asp Phe Met Thr Pro 140 145 150 155	1444
aaa gct cgt ctt gtc acg gtg aaa cgc aat gca agt cgc gat gaa att Lys Ala Arg Leu Val Thr Val Lys Arg Asn Ala Ser Arg Asp Glu Ile 160 165 170	1492
ttt ggt cta atg cat aca cac cgt gta gaa aaa gtc ctt gtt gtc agc Phe Gly Leu Met His Thr His Arg Val Glu Lys Val Leu Val Val Ser 175 180 185	1540
gac gat ttc aaa tta aaa ggc atg atc acc tta aaa gac tac caa aaa Asp Asp Phe Lys Leu Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys 190 195 200	1588
tcc gag caa aaa cca caa gcc tgt aaa gat gaa ttt ggt cgt tta cgt Ser Glu Gln Lys Pro Gln Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg 205 210 215	1636
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gca tta gtg aaa gca ggg gtc gat gtg tta ttg att gac tca tca cac Ala Leu Val Lys Ala Gly Val Asp Val Leu Leu Ile Asp Ser Ser His 240 245 250	1732
ggt cat tca gaa ggt gtg tta caa cgt gtg cgt gaa act cgt gcg aaa Gly His Ser Glu Gly Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys 255 260 265	1780
tac cca gat ttg cca att gtt gca ggt aat gtg gca acc gct gaa ggc Tyr Pro Asp Leu Pro Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly 270 275 280	1828

gca att gcg ttg gct gat gca ggg gca agt gca gtg aaa gtg ggg att Ala Ile Ala Leu Ala Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile 285 290 295	1876
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cttaaagcac aagtggcga tgatgaagtg attttaggct tatctgggttgc cgtaactgc 4610
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<210> 24
<211> 487
<212> PRT
<213> Pasteurella multocida

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20 25 30
Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro Met Leu Ser Ala Ala
35 40 45
Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile Ser Leu Ala Gln Glu
50 55 60
Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser Ile Glu Arg Gln Ala
65 70 75 80
Glu Arg Val Arg Lys Val Lys Lys Phe Glu Ser Gly Ile Val Ser Asp
85 90 95
Pro Val Thr Val Ser Pro Thr Leu Ser Leu Ala Glu Leu Ser Glu Leu
100 105 110
Val Lys Lys Asn Gly Phe Ala Ser Phe Pro Val Val Asp Asp Glu Lys
115 120 125
Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr Arg Phe Val Thr Asp
130 135 140
Leu Asn Lys Thr Val Ala Asp Phe Met Thr Pro Lys Ala Arg Leu Val
145 150 155 160
Thr Val Lys Arg Asn Ala Ser Arg Asp Glu Ile Phe Gly Leu Met His
165 170 175
Thr His Arg Val Glu Lys Val Leu Val Val Ser Asp Asp Phe Lys Leu
180 185 190
Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys Ser Glu Gln Lys Pro
195 200 205
Gln Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg Val Gly Ala Ala Val
210 215 220
Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp Ala Leu Val Lys Ala
225 230 235 240
Gly Val Asp Val Leu Leu Ile Asp Ser Ser His Gly His Ser Glu Gly
245 250 255
Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys Tyr Pro Asp Leu Pro
260 265 270
Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly Ala Ile Ala Leu Ala
275 280 285
Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile Gly Pro Gly Ser Ile
290 295 300

Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val Pro Gln Ile Thr Ala
 305 310 315 320

Ile Ala Asp Ala Ala Glu Ala Leu Lys Asp Arg Gly Ile Pro Val Ile
 325 330 335

Ala Asp Gly Gly Ile Arg Phe Ser Gly Asp Ile Ser Lys Ala Ile Ala
 340 345 350

Ala Gly Ala Ser Cys Val Met Val Gly Ser Met Phe Ala Gly Thr Glu
 355 360 365

Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly Arg Ala Phe Lys Ser
 370 375 380

Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser Lys Gly Ser Ser Asp
 385 390 395 400

Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys Leu Val Pro Glu Gly
 405 410 415

Ile Glu Gly Arg Ile Pro Tyr Lys Gly Phe Leu Lys Glu Ile Ile His
 420 425 430

Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly Leu Thr Gly Cys Ala
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Thr Ile Asp Glu Leu Arg Thr Lys Ala Gln Phe Val Arg Ile Ser Gly
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 aattgacggc gattttagggc gtgatgaatt tggatgacggc gatttataaca gtatggcg 180
 gagataaaaa atg gcg aag aaa aag aaa tta caa caa gcg aaa aaa 229
 Met Ala Lys Lys Lys Lys Leu Gln Gln Ala Lys Lys
 1 5 10

gta caa gtt ggc tta gat aca caa aca aat gag gcg cgt gtc acg gag 277
 Val Gln Val Gly Leu Asp Thr Gln Thr Asn Glu Ala Arg Val Thr Glu
 15 20 25

aca gga aga att att tct gat cac cca agc aat aaa att acc ccc gca		325
Thr Gly Arg Ile Ile Ser Asp His Pro Ser Asn Lys Ile Thr Pro Ala		
30	35	40
		45
aag tta aaa ggg att tta gaa gat gct gaa ggt ggt gat att acc gcg		373
Lys Leu Lys Gly Ile Leu Glu Asp Ala Glu Gly Gly Asp Ile Thr Ala		
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caa cat gag ctt ttc atg gat att gaa gaa cgc gac agt tgc atc ggg		421
Gln His Glu Leu Phe Met Asp Ile Glu Glu Arg Asp Ser Cys Ile Gly		
65	70	75
gca aat att caa acc cgt aag cgt gcg att tta acc ctt gac tgg cgc		469
Ala Asn Ile Gln Thr Arg Lys Arg Ala Ile Leu Thr Leu Asp Trp Arg		
80	85	90
att gca gag cca cgt aat gcc aca ccg caa gaa gaa aaa ctg caa gtc		517
Ile Ala Glu Pro Arg Asn Ala Thr Pro Gln Glu Lys Leu Gln Val		
95	100	105
gaa att gac gag ctt ttc tat caa ttc cca atg cta gaa gat tta atg		565
Glu Ile Asp Glu Leu Phe Tyr Gln Phe Pro Met Leu Glu Asp Leu Met		
110	115	120
		125
gtg gat atg atg gat gcg gta gga cat ggt ttt tcg gcg tta gaa att		613
Val Asp Met Met Asp Ala Val Gly His Gly Phe Ser Ala Leu Glu Ile		
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gaa tgg aag caa gct gaa agt aaa tgg att cca gtt aat ttt atc gca		661
Glu Trp Lys Gln Ala Glu Ser Lys Trp Ile Pro Val Asn Phe Ile Ala		
145	150	155
cgt ccg cag tcg tgg ttt aaa cta gac aag gat gat aat tta ctg ctt		709
Arg Pro Gln Ser Trp Phe Lys Leu Asp Lys Asp Asp Asn Leu Leu Leu		
160	165	170
aaa acg cca gat aat caa gac ggt gag ccg ttg aga caa tat ggc tgg		757
Lys Thr Pro Asp Asn Gln Asp Gly Glu Pro Leu Arg Gln Tyr Gly Trp		
175	180	185
gta gtg cat acc cac aaa tca aga aca gta cag ctt gct cgt atg ggt		805
Val Val His Thr His Lys Ser Arg Thr Val Gln Leu Ala Arg Met Gly		
190	195	200
		205
tta ttt aga acg ctc gca tgg ctt tat atg ttt aaa cac tac tcg gtg		853
Leu Phe Arg Thr Leu Ala Trp Leu Tyr Met Phe Lys His Tyr Ser Val		
210	215	220
cat gat ttt gcc gaa ttt cta gag ctt tat ggt atg ccg att cgt att		901
His Asp Phe Ala Glu Phe Leu Glu Leu Tyr Gly Met Pro Ile Arg Ile		
225	230	235
ggt aaa tac cca ttt ggg gca acg aat gac gaa aag cgc aca tta ttg		949
Gly Lys Tyr Pro Phe Gly Ala Thr Asn Asp Glu Lys Arg Thr Leu Leu		
240	245	250
cgt gca ctt gct caa atc gga cat aac gca gca ggg att atg cca gaa		997
Arg Ala Leu Ala Gln Ile Gly His Asn Ala Ala Gly Ile Met Pro Glu		
255	260	265
gga atg aat gtt gag ttg cat aat gtg aca aac act act ggc tcg gct		1045
Gly Met Asn Val Glu Leu His Asn Val Thr Asn Thr Thr Gly Ser Ala		
270	275	280
		285

gga aac aac ccg ttt ttg caa atg gtg gac tgg tgt gaa aag tcc gcc Gly Ser Asn Pro Phe Leu Gln Met Val Asp Trp Cys Glu Lys Ser Ala 290 295 300	1093
gca cgt ttg att cta ggg caa aca aca agc ggt gca gat ggt aaa Ala Arg Leu Ile Leu Gly Gln Thr Leu Thr Ser Gly Ala Asp Gly Lys 305 310 315	1141
act tca act aat gcc ctt gga caa gtg cat aat gaa gtc aga cgt gac Thr Ser Thr Asn Ala Leu Gly Gln Val His Asn Glu Val Arg Arg Asp 320 325 330	1189
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tct cgt gtg ccg tat ttc gag ttt gac acg aaa gaa tat gct gat tta Ser Arg Val Pro Tyr Phe Glu Phe Asp Thr Lys Glu Tyr Ala Asp Leu 370 375 380	1333
agt gtc cta gcg gat gct att cct aag ctt gtg agc gta gga gtg cgc Ser Val Leu Ala Asp Ala Ile Pro Lys Leu Val Ser Val Gly Val Arg 385 390 395	1381
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tct gcg aat aat aac agt tct act gcg cag ggc gtg cta gat ggt gga Ser Ala Asn Asn Ser Ser Thr Ala Gln Gly Val Leu Asp Gly Gly 465 470 475	1621
ctt gcg caa gca ttt aat gag cct gat ttt aat aaa caa tta aat cca Leu Ala Gln Ala Phe Asn Glu Pro Asp Phe Asn Lys Gln Leu Asn Pro 480 485 490	1669
atg gta aag aaa gct gtt gcg gta ctc atg gca tgt gac tct tac gat Met Val Lys Lys Ala Val Ala Val Leu Met Ala Cys Asp Ser Tyr Asp 495 500 505	1717
gag gcg gca gaa aaa ctc gct gaa gca tac cca gaa att tca agt cac Glu Ala Ala Glu Lys Leu Ala Glu Ala Tyr Pro Glu Ile Ser Ser His 510 515 520 525	1765
gaa cac gaa cag tat ctc tca aat gcg ctg ttt tta gct gat tta ctt Glu His Glu Gln Tyr Leu Ser Asn Ala Leu Phe Leu Ala Asp Leu Leu 530 535 540	1813

gga gga act aat gtc taaaccgctt agttttctat tcggacttga accaacgcaa 1868
 Gly Gly Thr Asn Val
 545

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 catgatagtg ccatcgcaag agctacaaca atcgcgagat tatcttagtct tgagatgacg 1988
 aatgatattt ataaatcaat ggaagttgcc aaaaaagagg gtaagagctt tacacaatgg 2048
 aaaaaagact tggtaagtga gtttgagaaa aaaggctggg tattcggca tgataaatct 2108
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 cgctatcagc gcatgatgga taatattgat catcgcccct attggcaata ttccgctgtc 2288
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<213> Pasteurella multocida

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Ile	Ile	Ser	Asp	His	Pro	Ser	Asn	Lys	Ile	Thr	Pro	Ala	Lys	Leu	Lys
	35					40						45			

Gly	Ile	Leu	Glu	Asp	Ala	Glu	Gly	Asp	Ile	Thr	Ala	Gln	His	Glu
	50				55				60					

Leu	Phe	Met	Asp	Ile	Glu	Glu	Arg	Asp	Ser	Cys	Ile	Gly	Ala	Asn	Ile
	65				70				75					80	

Gln	Thr	Arg	Lys	Arg	Ala	Ile	Leu	Thr	Leu	Asp	Trp	Arg	Ile	Ala	Glu
	85					90						95			

Pro	Arg	Asn	Ala	Thr	Pro	Gln	Glu	Glu	Lys	Leu	Gln	Val	Glu	Ile	Asp
	100					105				110					

Glu	Leu	Phe	Tyr	Gln	Phe	Pro	Met	Leu	Glu	Asp	Leu	Met	Val	Asp	Met
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Met	Asp	Ala	Val	Gly	His	Gly	Phe	Ser	Ala	Leu	Glu	Ile	Glu	Trp	Lys
	130				135						140				

Gln	Ala	Glu	Ser	Lys	Trp	Ile	Pro	Val	Asn	Phe	Ile	Ala	Arg	Pro	Gln
	145					150			155				160		

Ser	Trp	Phe	Lys	Leu	Asp	Lys	Asp	Asp	Asn	Leu	Leu	Leu	Lys	Thr	Pro
	165					170				175					

Asp Asn Gln Asp Gly Glu Pro Leu Arg Gln Tyr Gly Trp Val Val His
 180 185 190
 Thr His Lys Ser Arg Thr Val Gln Leu Ala Arg Met Gly Leu Phe Arg
 195 200 205
 Thr Leu Ala Trp Leu Tyr Met Phe Lys His Tyr Ser Val His Asp Phe
 210 215 220
 Ala Glu Phe Leu Glu Leu Tyr Gly Met Pro Ile Arg Ile Gly Lys Tyr
 225 230 235 240
 Pro Phe Gly Ala Thr Asn Asp Glu Lys Arg Thr Leu Leu Arg Ala Leu
 245 250 255
 Ala Gln Ile Gly His Asn Ala Ala Gly Ile Met Pro Glu Gly Met Asn
 260 265 270
 Val Glu Leu His Asn Val Thr Asn Thr Thr Gly Ser Ala Gly Ser Asn
 275 280 285
 Pro Phe Leu Gln Met Val Asp Trp Cys Glu Lys Ser Ala Ala Arg Leu
 290 295 300
 Ile Leu Gly Gln Thr Leu Thr Ser Gly Ala Asp Gly Lys Thr Ser Thr
 305 310 315 320
 Asn Ala Leu Gly Gln Val His Asn Glu Val Arg Arg Asp Leu Leu Val
 325 330 335
 Ser Asp Ala Lys Gln Ile Ala Gln Thr Ile Thr Gln Gln Ile Ile Leu
 340 345 350
 Pro Tyr Leu Gln Ile Asn Ile Asp Pro Asn Ile Leu Pro Ser Arg Val
 355 360 365
 Pro Tyr Phe Glu Phe Asp Thr Lys Glu Tyr Ala Asp Leu Ser Val Leu
 370 375 380
 Ala Asp Ala Ile Pro Lys Leu Val Ser Val Gly Val Arg Ile Pro Glu
 385 390 395 400
 Asn Trp Val Arg Asp Lys Ala Gly Ile Pro Glu Pro Gln Glu Asn Glu
 405 410 415
 Thr Ile Leu Ser Ala Val Gln His Asp Phe Lys Thr Asp Leu Asn Asp
 420 425 430
 Val Glu Asn Pro Lys Lys Gln Thr Ala Leu Ser Val Gln Asn His Val
 435 440 445
 Thr Gly Cys Gln Cys Asp Gly Cys Arg Gly Val Ala Leu Ser Ala Asn
 450 455 460
 Asn Asn Ser Ser Thr Ala Gln Gly Val Leu Asp Gly Gly Leu Ala Gln
 465 470 475 480
 Ala Phe Asn Glu Pro Asp Phe Asn Lys Gln Leu Asn Pro Met Val Lys
 485 490 495
 Lys Ala Val Ala Val Leu Met Ala Cys Asp Ser Tyr Asp Glu Ala Ala
 500 505 510

Glu Lys Leu Ala Glu Ala Tyr Pro Glu Ile Ser Ser His Glu His Glu
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Gln Tyr Leu Ser Asn Ala Leu Phe Leu Ala Asp Leu Leu Gly Gly Thr
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Asn Val
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ttt tta gaa gat cgc cgt gaa aag ctt acc gaa gaa aaa aca tta 97
 Phe Leu Glu Asp Arg Arg Glu Lys Lys Leu Thr Glu Lys Thr Leu
 20 25 30

ggg ctt agt gat gca gtg cgt ttt gct aat gat caa acc cct tat ctc 145
 Gly Leu Ser Asp Ala Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu
 35 40 45

cgt tat ggt att gaa tat cga tat aac ggc ttg tct tgg ttg gaa acg 193
 Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr
 50 55 60

gta aag ctt ttt ttg gca aag cag aaa atc gaa caa cgt tct gct ctc 241
 Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu
 65 70 75 80

caa gag ttt gat att aat aat agg aat aaa ttg gat tcg act atg tcg Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser 85 90 95	289
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agt cct tta tat tgg ggg ccg agt cgc cat cgt tta tnt gcg aaa ttc Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe 115 120 125	385
gaa ttt cgt gat ang ttt tta gaa aat atg aat aag cnt ttt acg ttt Glu Phe Arg Asp Xaa Phe Leu Glu Asn Met Asn Lys Xaa Phe Thr Phe 130 135 140	433
cg ^g ccg tgg caa atc aat ana ttc aga caa caa ggt cga aat aac tat Arg Pro Trp Gln Ile Asn Xaa Phe Arg Gln Gln Gly Arg Asn Asn Tyr 145 150 155 160	481
aca gaa gtg ttt ccc gtt aaa tcc cga gag ttt tct ttt tct ctt atg Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met 165 170 175	529
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tgg gat cac tat aac tat aag cca tta tta aat tct cag cat aat atc Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile 195 200 205	625
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tac cgt tta agt acc ggt ttt agg gtt ccc cgt gtt gaa gat ctt tat Tyr Arg Leu Ser Thr Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr 245 250 255	769
ttt gaa gac cga gga aaa agt tct tca caa ttt ctt cct aac ccc gat Phe Glu Asp Arg Gly Lys Ser Ser Gln Phe Leu Pro Asn Pro Asp 260 265 270	817
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aat caa tat gcc cat ttc agc gtc ggg ctt ttc cgt aca cgt tat cat Asn Gln Tyr Ala His Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His 290 295 300	913
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Leu Asn Gly Ser Ala Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu	
355	360
365	
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Lys Gly Ser Tyr Ser Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys	
370	375
380	
tct att caa cca tgg aca gtg gta acc ggt att gat tac gaa act gaa	1201
Ser Ile Gln Pro Trp Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu	
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Gly Trp Ser Val Ser Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala	
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Lys Asp Ala Ile Glu Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys	
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Gly Leu Ser Asp Ala Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu
 35 40 45

Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr
 50 55 60

Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu
 65 70 75 80

Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser
 85 90 95

Phe Val Tyr Leu Gln Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr
 100 105 110

Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe
 115 120 125

Glu Phe Arg Asp Xaa Phe Leu Glu Asn Met Asn Lys Xaa Phe Thr Phe
 130 135 140

Arg Pro Trp Gln Ile Asn Xaa Phe Arg Gln Gln Gly Arg Asn Asn Tyr
 145 150 155 160

Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met
 165 170 175

Asp Asp Ile Lys Ile Gly Glu Leu Leu His Leu Gly Leu Gly Arg
 180 185 190

Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile
 195 200 205

Asn Arg Thr Gln Arg Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser
 210 215 220

Tyr Gln Leu Ser Leu Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala
 225 230 235 240

Tyr Arg Leu Ser Thr Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr
 245 250 255

Phe Glu Asp Arg Gly Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp
 260 265 270

Leu Gln Pro Glu Thr Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln
 275 280 285

Asn Gln Tyr Ala His Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His
 290 295 300

Asn Phe Ile Gln Glu Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu
 305 310 315 320

Tyr Asn Arg Thr Tyr Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe
 325 330 335

Val Asn Glu Pro Glu Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala
 340 345 350

Leu Asn Gly Ser Ala Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu
355 360 365

Lys Gly Ser Tyr Ser Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys
370 375 380

Ser Ile Gln Pro Trp Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu
385 390 395 400

Gly Trp Ser Val Ser Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala
405 410 415

Lys Asp Ala Ile Glu Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys
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Gln Trp Pro His Leu Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly
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Gln Val
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act ttc aac atc gaa aat aat ctg tca tat ggt gga gtt tat tct cgg		6327
Thr Phe Asn Ile Glu Asn Asn Leu Ser Tyr Gly Gly Val Tyr Ser Arg		
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Ile Glu Lys Glu Met Ile Asn Lys Ala Gly Tyr Glu Gly Arg Asn Pro		
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act tgg tgg gct gat aga att tta ggg caa agt agt tac tgt ggt tat		6423
Thr Trp Trp Ala Asp Arg Ile Leu Gly Gln Ser Ser Tyr Cys Gly Tyr		
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Asn Ala Leu Lys Cys Pro Lys His Glu Pro Leu Thr Ser Phe Leu Ile		
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cca gtt gaa gca acg aca cag tca tta tat ttt gca aat att ctt aag		6519
Pro Val Glu Ala Thr Thr Gln Ser Leu Tyr Phe Ala Asn Ile Leu Lys		
575	580	585
gta cat aat atg att agc ata gat tta gga tat cgt tat gat cat att		6567
Val His Asn Met Ile Ser Ile Asp Leu Gly Tyr Arg Tyr Asp His Ile		
590	595	600
aaa tat aac cct gaa tac act cca gga gta act cca aaa att cca gat		6615
Lys Tyr Asn Pro Glu Tyr Thr Pro Gly Val Thr Pro Lys Ile Pro Asp		
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Asp Met Val Lys Gly Leu Phe Ile Pro Met Pro Lys Glu Pro Gln Leu		
620	625	630
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Lys Asp Phe Asp Tyr Asn Tyr Ala Lys Phe Gly Glu Ala Tyr Lys Lys		
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tgg aaa gaa tat ctg cca aaa aat gcg gaa gaa aat att gct tac att		6759
Trp Lys Glu Tyr Leu Pro Lys Asn Ala Glu Glu Asn Ile Ala Tyr Ile		
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Ala Gln Asp Lys Thr Phe Lys Lys His Ser Tyr Ser Leu Gly Ala Thr		
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Phe Asp Pro Leu Asn Phe Leu Arg Val Gln Val Lys Tyr Ser Lys Gly		
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Phe Arg Ala Pro Thr Ser Asp Glu Leu Tyr Phe Thr Phe Lys His Pro		
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gat ttt acg att tta ccg aac ccc gtg ttg aaa cca gag gaa gca aaa		6951
Asp Phe Thr Ile Leu Pro Asn Pro Val Leu Lys Pro Glu Glu Ala Lys		
715	720	725
730		
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Asn Gln Glu Ile Ala Leu Thr Val His Asp Asn Trp Gly Phe Val Ser		
735	740	745

aca agt gtt ttc caa aca aag tat cgt cat ttt att gat tta gcg tat	7047
Thr Ser Val Phe Gln Thr Lys Tyr Arg His Phe Ile Asp Leu Ala Tyr	
750	755
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tta ggt tca aga aat tta tcg aat tcc gtg gga ggg cag gca caa gca	7095
Leu Gly Ser Arg Asn Leu Ser Asn Ser Val Gly Gly Gln Ala Gln Ala	
765	770
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aga gat ttc caa gtt tat caa aat gtc aat gtc gat aat gcc aaa gtt	7143
Arg Asp Phe Gln Val Tyr Gln Asn Val Asn Val Asp Asn Ala Lys Val	
780	785
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aaa gga ctt gaa att aat gca cgt ttg aat ttg gga tat ttt tgg cat	7191
Lys Gly Leu Glu Ile Asn Ala Arg Leu Asn Leu Gly Tyr Phe Trp His	
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Val Leu Asp Gly Phe Asn Thr Ser Tyr Lys Phe Thr Tyr Gln Arg Gly	
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Arg Leu Asp Gly Asp Arg Pro Met Asn Ala Ile Gln Pro Lys Ala Ser	
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Val Phe Gly Leu Gly Tyr Asp His Lys Glu Asn Lys Phe Gly Ala Asp	
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Leu Tyr Ile Thr Arg Val Ser Glu Lys Lys Ala Lys Asp Thr Tyr Asn	
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	890
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Lys Asn Leu Thr Leu Gln Phe Gly Val Tyr Asn Leu Thr Asp Arg Lys	
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tac ttg aca tgg gaa tct gct cgt tcg att aaa cca ttt ggt aca agt	7575
Tyr Leu Thr Trp Glu Ser Ala Arg Ser Ile Lys Pro Phe Gly Thr Ser	
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	935
aat tta att aat caa aaa aca ggc gca gga att aat cgt ttt tac tca	7623
Asn Leu Ile Asn Gln Lys Thr Gly Ala Gly Ile Asn Arg Phe Tyr Ser	
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Pro Gly Arg Asn Phe Lys Leu Ser Ala Glu Ile Thr Phe	
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 35 40 45

Glu Lys Lys Ile Gly Glu Thr Val Lys Thr Ala Ser Gln Leu Lys Arg
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Gln Gln Val Gln Asp Ser Arg Asp Leu Val Arg Tyr Glu Thr Gly Val
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Thr Val Val Glu Ala Gly Arg Phe Gly Ser Ser Gly Tyr Ala Ile Arg
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Gly Val Asp Glu Asn Arg Val Ala Ile Thr Val Asp Gly Leu His Gln
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Ala Glu Thr Leu Ser Ser Gln Gly Phe Lys Glu Leu Phe Glu Gly Tyr
 115 120 125

Gly Asn Phe Asn Asn Thr Arg Asn Ser Val Glu Ile Glu Thr Leu Lys
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Val Ala Lys Ile Ala Lys Gly Ala Asp Ser Val Lys Val Gly Ser Gly
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Ser Leu Gly Gly Ala Val Leu Phe Glu Thr Lys Asp Ala Arg Asp Phe
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Leu Thr Glu Lys Asp Trp His Ile Gly Tyr Lys Ala Gly Tyr Ser Thr
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Ala Asp Asn Gln Gly Leu Asn Ala Val Thr Leu Ala Gly Arg Tyr Gln
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Met Phe Asp Ala Leu Ile Met His Ser Lys Arg His Gly His Glu Leu
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Glu Asn Tyr Asp Tyr Lys Asn Gly Arg Asp Ile Gln Gly Lys Glu Arg
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Glu Lys Ala Asp Pro Tyr Thr Ile Thr Lys Glu Ser Thr Leu Val Lys
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Phe Ser Phe Ser Pro Thr Glu Asn His Arg Phe Thr Val Ala Ser Asp
 260 265 270

Thr Tyr Leu Gln His Ser Arg Gly His Asp Leu Ser Tyr Asn Leu Val
 275 280 285

Ala Thr Thr His Ile Gln Leu Asp Glu Lys Glu Ser Arg His Ala Asn
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 Val Thr Pro Phe Trp Asp Thr Leu Lys Leu Ser Tyr Ser Gln Gln Arg
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 Cys Asp Ser Tyr Lys Asn Pro Leu Gly Leu Gln Phe Lys Asp Gly Gln
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 450 455 460
 Glu Gly Gly Leu Pro Asn Tyr Leu Ile Leu Pro Asn Ser Lys Gly Tyr
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 485 490 495
 Ile Asn Leu Asp Leu Thr Lys Thr Phe Leu Thr Phe Asn Ile Glu Asn
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 Gln Ser Leu Tyr Phe Ala Asn Ile Leu Lys Val His Asn Met Ile Ser
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 Ile Asp Leu Gly Tyr Arg Tyr Asp His Ile Lys Tyr Asn Pro Glu Tyr
 595 600 605
 Thr Pro Gly Val Thr Pro Lys Ile Pro Asp Asp Met Val Lys Gly Leu
 610 615 620
 Phe Ile Pro Met Pro Lys Glu Pro Gln Leu Lys Asp Phe Asp Tyr Asn
 625 630 635 640

Tyr Ala Lys Phe Gly Glu Ala Tyr Lys Lys Trp Lys Glu Tyr Leu Pro
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 675 680 685
 Leu Arg Val Gln Val Lys Tyr Ser Lys Gly Phe Arg Ala Pro Thr Ser
 690 695 700
 Asp Glu Leu Tyr Phe Thr Phe Lys His Pro Asp Phe Thr Ile Leu Pro
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 Asn Pro Val Leu Lys Pro Glu Glu Ala Lys Asn Gln Glu Ile Ala Leu
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 Thr Val His Asp Asn Trp Gly Phe Val Ser Thr Ser Val Phe Gln Thr
 740 745 750
 Lys Tyr Arg His Phe Ile Asp Leu Ala Tyr Leu Gly Ser Arg Asn Leu
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 Ser Asn Ser Val Gly Gly Gln Ala Gln Ala Arg Asp Phe Gln Val Tyr
 770 775 780
 Gln Asn Val Asn Val Asp Asn Ala Lys Val Lys Gly Leu Glu Ile Asn
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 Ala Arg Leu Asn Leu Gly Tyr Phe Trp His Val Leu Asp Gly Phe Asn
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 Thr Ser Tyr Lys Phe Thr Tyr Gln Arg Gly Arg Leu Asp Gly Asp Arg
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 Pro Met Asn Ala Ile Gln Pro Lys Ala Ser Val Phe Gly Leu Gly Tyr
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 Asp His Lys Glu Asn Lys Phe Gly Ala Asp Leu Tyr Ile Thr Arg Val
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 Ser Glu Lys Lys Ala Lys Asp Thr Tyr Asn Met Phe Tyr Lys Glu Gln
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 Gly Tyr Lys Asp Ser Ala Val Arg Trp Arg Ser Asp Asp Tyr Thr Leu
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 Phe Gly Val Tyr Asn Leu Thr Asp Arg Lys Tyr Leu Thr Trp Glu Ser
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 Ala Arg Ser Ile Lys Pro Phe Gly Thr Ser Asn Leu Ile Asn Gln Lys
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 Thr Gly Ala Gly Ile Asn Arg Phe Tyr Ser Pro Gly Arg Asn Phe Lys
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 Leu Ser Ala Glu Ile Thr Phe
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Tyr Cys Phe Asp Lys Arg Ala Tyr Ile His Glu Leu Tyr Thr Glu Gln
 35 40 45

Glu Leu Ile Asp Arg Gly Ile Glu Tyr Val Val Ser Thr Met Pro Ser
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Gly Val Ile Lys Pro Asp Gly Thr Ile Lys Glu Val Lys Arg Tyr Thr
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Ser Val Glu Glu Phe Lys Gln Met Asn Pro Ala Cys Cys Thr Leu Thr
 85 90 95

Thr Phe Ile Asp Glu Gly Asp Gly Tyr Pro Asp Asp Asp Gly Tyr
 100 105 110

Gly Tyr Val Arg Ile Glu Tyr Leu Arg His Tyr Val Glu Asn Leu Lys
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Met Asn Ile Leu Phe Val Ser Asp Asp
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Val Tyr Ala Lys His Leu Val Val Ala Ile Lys Ser Ile Ile Asn His
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                           25

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gaa aat aag aga aat att aat gat att gtt tct tct tat gga agt gaa 495
Glu Asn Lys Arg Asn Ile Asn Asp Ile Val Ser Ser Tyr Gly Ser Glu
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gtc aac ttt att gct gtg aat gag aaa gaa ttt gag agt ttt cct gtt 543
Val Asn Phe Ile Ala Val Asn Glu Lys Glu Phe Glu Ser Phe Pro Val
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Gln Ile Ser Tyr Ile Ser Leu Ala Thr Tyr Ala Arg Leu Lys Ala Ala
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gag tat ttg ccg gat aat tta aat aaa att att tat tta gat gtt gat 639
Glu Tyr Leu Pro Asp Asn Leu Asn Lys Ile Ile Tyr Leu Asp Val Asp
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Val Leu Val Phe Asn Ser Leu Glu Met Leu Trp Asn Val Asp Val Asn																																																																																																													
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Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
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Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
65 70 75 80
Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu
85 90 95
Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu
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Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys
115 120 125
Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile
130 135 140

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 165 170 175
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 Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe
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 Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Xaa Gln Tyr His Lys Gly
 210 215 220
 Lys Xaa Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val
 225 230 235 240
 Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys
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 His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Xaa Xaa Ser Arg
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 <213> Pasteurella multocida

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  Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu
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nat aat aaa ggc att caa gat gag caa tta ttc atc gac acg ggg atg 145
  Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met
    35          40          45

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  Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser
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tct aaa gca aat caa att gaa gtg atc atc gct aac aac gat ggt atg 241
  Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met
    65          70          75          80

gcg atg ggg gca ttg gaa gcc acg aaa gca cat ggt aaa aaa tta cca 289
  Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro
    85          90          95

atc ttc ngt gta nat gcg tta cca gaa gtc ctc caa tta atc aaa aaa 337
  Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys
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  Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys
    115         120         125

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  Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr
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Cys Trp Cys Gly Cys Gly			
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<213> Pasteurella multocida

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Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu
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Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met
      35          40           45

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Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met
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Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro
      85          90           95

Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys
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Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys
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Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr
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 attacgcagt gaaaatgaac aactaaagag tgagcaccaa aactggcaag aacgtttacg 240
 ctcattatta ggcaaaaattg ataacgtata attcacttct tattaaggct tagttttct 300
 aagccttatt ttttaggaga aatta atg aaa aca aaa att tgt att atc act 352
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ggc agt acg ctt ggt gca gaa tat gtt gca gaa cat att gct gaa 400
 Gly Ser Thr Leu Gly Gly Ala Glu Tyr Val Ala Glu His Ile Ala Glu
 10 15 20 25

ata tta gaa caa caa gat tat cct gta cgt tta gaa cat gga cca aat 448
 Ile Leu Glu Gln Gln Asp Tyr Pro Val Arg Leu Glu His Gly Pro Asn
 30 35 40

ttt gaa gaa gtg atc gat gaa aaa tgt tgg ctt gtt gtc acc tct acc 496
 Phe Glu Glu Val Ile Asp Glu Lys Cys Trp Leu Val Val Thr Ser Thr
 45 50 55

cat ggt gca ggt gaa tta ccg gat aat att aaa cct ctg ttt gaa aaa 544
 His Gly Ala Gly Glu Leu Pro Asp Asn Ile Lys Pro Leu Phe Glu Lys
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tta gca ttt cac cca aaa cag tta gct gac tta cgc ttt gcg gtg atc 592
 Leu Ala Phe His Pro Lys Gln Leu Ala Asp Leu Arg Phe Ala Val Ile
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 90 95 100 105

gtg gaa caa tta ctg cta agc aaa gat gct tta caa ctg tgt gaa tcg 688
 Val Glu Gln Leu Leu Ser Lys Asp Ala Leu Gln Leu Cys Glu Ser
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cta aga atg gat atg cta acc att act gat cct gaa cac acg gcc gaa 736
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<213> Pasteurella multocida

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Pro Val Arg Leu Glu His Gly Pro Asn Phe Glu Glu Val Ile Asp Glu
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Lys Cys Trp Leu Val Val Thr Ser Thr His Gly Ala Gly Glu Leu Pro
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Asp Asn Ile Lys Pro Leu Phe Glu Lys Leu Ala Phe His Pro Lys Gln
 65 70 75 80

Leu Ala Asp Leu Arg Phe Ala Val Ile Gly Leu Gly Asn Ser Asp Tyr
 85 90 95

Asp Thr Phe Cys His Ala Val Asp His Val Glu Gln Leu Leu Ser
 100 105 110

Lys Asp Ala Leu Gln Leu Cys Glu Ser Leu Arg Met Asp Met Leu Thr
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<213> Pasteurella multocida

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 Pro Val Ser Thr Ala Thr Gly Ser Met Val Ile Asp Ile Gly Gly Gly
 155 160 165 170

acg acg gaa gtt gcg gtg att tct tta aat ggc att gtg tat tcc tct 3760
 Thr Thr Glu Val Ala Val Ile Ser Leu Asn Gly Ile Val Tyr Ser Ser
 175 180 185

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205	210	215	
atc aaa caa gag att ggt agt gcg ttt att caa gaa ggc gat gaa gtc	3904		
Ile Lys Gln Glu Ile Gly Ser Ala Phe Ile Gln Glu Gly Asp Glu Val			
220	225	230	
cgt gaa att gaa gtg cat ggt cat aac tta gca gaa ggt gcg ccg cgt	3952		
Arg Glu Ile Glu Val His Gly His Asn Leu Ala Glu Gly Ala Pro Arg			
235	240	245	250
tct ttc aaa ctc acc tca cgt gat gtg tta gaa gct att caa gcc ccg	4000		
Ser Phe Lys Leu Thr Ser Arg Asp Val Leu Glu Ala Ile Gln Ala Pro			
255	260	265	
tta aat ggc att gtt gcg gca gtg cgc acg gcc ttg gaa gag tgt caa	4048		
Leu Asn Gly Ile Val Ala Ala Val Arg Thr Ala Leu Glu Glu Cys Gln			
270	275	280	
cca gaa cat gct gcg gat att ttt gaa cgt ggc atg gtc tta act ggt	4096		
Pro Glu His Ala Ala Asp Ile Phe Glu Arg Gly Met Val Leu Thr Gly			
285	290	295	
ggc ggt gcc ctt att cgt aat att gat gtt tta ctg tca aaa gaa acc	4144		
Gly Gly Ala Leu Ile Arg Asn Ile Asp Val Leu Leu Ser Lys Glu Thr			
300	305	310	
ggt ggt ggc gag gca tta gag atg atc gat atg cac ggt ggt gat att	4192		
Gly Gly Glu Ala Leu Glu Met Ile Asp Met His Gly Gly Asp Ile			
335	340	345	
ttt agt gac gat atc taatatgatt taaaagtgcg gtgatattag accgcacttt	4240		
Phe Ser Asp Asp Ile			
350			
tacttctt ttattgctga caaggcttagc ctaattcgta tatgaaacct attttgaa	4355		
aagcacctcc ttttaggtctt cgcttaattc tggcgatttt agcatccatt gcattgattt	4415		
tttcggacgg tcaatccaat gcgatgatta aagcacgcag tattatggaa accgcagtag	4475		
gcgggctgta ttatcttgcc aatacaccga gaacggattt ggatgggtt tcagataatt	4535		
tggttgatac caataaattt caaattgaaa accgagtttt gcgtgatcaa ctgcgtgaaa	4595		
aaaatgcaga tttattgtt ttagatcaac tcaaagttaga aaatcaacgc ctgcgttat	4655		
tgcttaattc ccctctacgt acagatgagt ataaaaaaat tgctgaagtt ttaacggcag	4715		
aaactgatgt gtatcgtaag caagtcgtga ttaaccaagg acaacgtgac ggtgctttag	4775		
tcgggcagcc gattattgtat gaaaagggtt ttgttggca acttatctcc gtttgtgaaa	4835		
atacgagtcg cgttcttcta ttgacagatg tgactcattc tattccagta caagtactac	4895		

245	250	255
Arg Asp Val Leu Glu Ala Ile Gln Ala Pro Leu Asn Gly Ile Val Ala		
260	265	270

Ala Val Arg Thr Ala Leu Glu Glu Cys Gln Pro Glu His Ala Ala Asp		
275	280	285

Ile Phe Glu Arg Gly Met Val Leu Thr Gly Gly Ala Leu Ile Arg		
290	295	300

Asn Ile Asp Val Leu Leu Ser Lys Glu Thr Gly Val Pro Val Ile Ile		
305	310	315
		320

Ala Asp Asp Pro Leu Thr Cys Val Ala Arg Gly Gly Glu Ala Leu		
325	330	335

Glu Met Ile Asp Met His Gly Gly Asp Ile Phe Ser Asp Asp Ile		
340	345	350

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<213> Pasteurella multocida

<220>

<221> CDS

<222> (1)...(1464)

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<223> pnp

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Thr Arg Val Gly Ile Gly Trp His Leu Asn Pro Asn Thr Ala Leu Ile		
1	5	10
		15

gaa aaa gtg aaa gcg att gca gaa gcg cgt tta ggc gaa gca tac cgt		96
Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly Glu Ala Tyr Arg		
20	25	30

atc act gaa aac aag cac gtt atg aac aaa att gat gcg att aaa gct		144
Ile Thr Glu Asn Lys His Val Met Asn Lys Ile Asp Ala Ile Lys Ala		
35	40	45

gat gtg att gca caa atc aca gct gaa gta gca gaa ggc gaa gac atc		192
Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu Gly Glu Asp Ile		
50	55	60

agt gaa ggg aaa att gtc gat att ttc acc gca ctt gaa agc caa atc		240
Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu Glu Ser Gln Ile		
65	70	75
		80

gta cgt agc cgt atc att gct ggt gaa cca cgt att gat ggt cgt aca		288
Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr		
85	90	95

gtg gat act gtt cgt gca tta gat att tgt act ggt gtt tta cca cgt		336
Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly Val Leu Pro Arg		
100	105	110

aca cac ggt tct gcg att ttc acc cgt ggt gaa aca cag gcg tta gct		384
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Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala			
115	120	125	
gtc gcg aca tta ggt aca gaa cgt gat gca caa att att gat gaa tta	432		
Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu			
130	135	140	
aca ggt gag cgt tca gat cac ttc tta ttc cac tac aac ttc ccg cca	480		
Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr Asn Phe Pro Pro			
145	150	155	160
tat tct gtg ggt gaa acc ggt atg att ggt tca cca aaa cgt cgt gaa	528		
Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro Lys Arg Arg Glu			
165	170	175	
att ggt cat ggt tta gcg aaa cgc ggt gta gct gca gtg atg cca	576		
Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala Ala Val Met Pro			
180	185	190	
aca ctt gcc gag ttc ccg tat gtg gta cgt gtt gtc tct gaa atc aca	624		
Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr			
195	200	205	
gaa tca aat ggt tct tct atg gca tcg gtt tgt ggt gcg tct tta	672		
Glu Ser Asn Gly Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu			
210	215	220	
gca tta atg gat gcg ggt gta cca att aaa gcg gcg gtt gca ggt att	720		
Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile			
225	230	235	240
gca atg ggc tta gtc aaa gaa gac gaa aaa ttt gtg gtg ctt tca gac	768		
Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp			
245	250	255	
atc tta ggt gat gaa gat cac tta ggt gac atg gac ttc aaa gtc gcg	816		
Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala			
260	265	270	
ggt aca cgt acg ggt gtg acg gca tta caa atg gat atc aaa atc gaa	864		
Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu			
275	280	285	
ggt atc aca gca gaa atc atg caa att gcg tta aac caa gcg aaa agc	912		
Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn Gln Ala Lys Ser			
290	295	300	
gca cgt tta cac att tta ggt gtg atg gag caa gcg atc cca gcg cca	960		
Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro			
305	310	315	320
cgt gcg gat att tct gat ttt gca ccg cgt att tac act atg aaa att	1008		
Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr Thr Met Lys Ile			
325	330	335	
gat ccg aag aaa atc aaa gat gtg atc ggt aaa ggt ggt gca acc att	1056		
Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Ala Thr Ile			
340	345	350	
cgt gcc tta aca gaa gaa aca ggt acc tca att gat atc gat gat gat	1104		
Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp Ile Asp Asp Asp			
355	360	365	

ggt acg gtg aag att gct gcg gtt gat ggc aat tca gca aaa gag gtg 1152
 Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser Ala Lys Glu Val
 370 375 380

 atg gcg cgt att gaa gat att act gca gaa gtt gaa gcg ggt gca gtg 1200
 Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu Ala Gly Ala Val
 385 390 395 400

 tat aaa ggt aaa gtt act cgt tta gct gat ttt ggt gcc ttc gtt tct 1248
 Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly Ala Phe Val Ser
 405 410 415

 atc gta ggt aac aaa gaa ggc tta gtg cat att tct caa atc gcg gaa 1296
 Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser Gln Ile Ala Glu
 420 425 430

 gag cgt gtt gag aaa gtg agt gat tat ctt gca gtg ggg caa gaa gtg 1344
 Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val Gly Gln Glu Val
 435 440 445

 act gtt aaa gtg gtt gag att gat cgt caa ggt cgt att cgt tta acc 1392
 Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr
 450 455 460

 atg aaa gaa gtt gca cca aag caa gaa cac gtt gat tct gtt gtc gca 1440
 Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp Ser Val Val Ala
 465 470 475 480

 gac gtt gcc gca gaa gaa aac gca taagcaataa acacccaacgc ctttcgttat 1494
 Asp Val Ala Ala Glu Glu Asn Ala
 485

 aaagggcgtt ggtgtcatg ttgataagta caatttgtgc ttttaaggcga agcgaaatga 1554
 agcaatttca tccgtggta aagtgcctgc taattttccc attttgggta tggtgtttaa 1614
 cagottgtgt taatcatgaa caagttttc tttcaaaaaga gaaattaatg tttagcagagc 1674
 aacatccgaa tgatcatctt gagcatgagg tgatggttgc gcaaatttagc gaattgttac 1734
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 acgatagctt aggattgtgg gcattggcgc gttatgattt tgaccaaaca ttagcgttgt 1854
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 acagcgcata tctagatatac tttaatgtgt tgtttgaact tgatcctcaa tatgagtatg 1974
 cattcctaaa tagagggcta aattttatt acgtcggacg ttatgaatta gctcagcggg 2034
 attttcttca attttatcaa gccgataaat cagatccata ccgcacttta tggctttatt 2094
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 <211> 488
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 <213> Pasteurella multocida

<400> 44

Thr Arg Val Gly Ile Gly Trp His Leu Asn Pro Asn Thr Ala Leu Ile
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Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly Glu Ala Tyr Arg
 20 25 30

Ile Thr Glu Asn Lys His Val Met Asn Lys Ile Asp Ala Ile Lys Ala
 35 40 45

Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu Gly Glu Asp Ile
 50 55 60

Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu Glu Ser Gln Ile
 65 70 75 80

Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr
 85 90 95

Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly Val Leu Pro Arg
 100 105 110

Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala
 115 120 125

Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu
 130 135 140

Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr Asn Phe Pro Pro
 145 150 155 160

Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro Lys Arg Arg Glu
 165 170 175

Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala Ala Val Met Pro
 180 185 190

Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr
 195 200 205

Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu
 210 215 220

Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile
 225 230 235 240

Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp
 245 250 255

Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala
 260 265 270

Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu
 275 280 285

Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn Gln Ala Lys Ser
 290 295 300

Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro
 305 310 315 320

Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr Thr Met Lys Ile
 325 330 335

Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile
 340 345 350

Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp Ile Asp Asp Asp
 355 360 365

Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser Ala Lys Glu Val
 370 375 380

Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu Ala Gly Ala Val
 385 390 395 400

Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly Ala Phe Val Ser
 405 410 415

Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser Gln Ile Ala Glu
 420 425 430

Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val Gly Gln Glu Val
 435 440 445

Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr
 450 455 460

Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp Ser Val Val Ala
 465 470 475 480

Asp Val Ala Ala Glu Glu Asn Ala
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<210> 45

<211> 633

<212> DNA

<213> Pasteurella multocida

<220>

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<222> (2)..(631)

<220>

<223> purF

<400> 45

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 Gly Glu Lys Ile Ala Arg Glu Trp Ala Asp Val Asp Asp Ile Asp Val
 20 25 30

gtc att cct gtg cct gaa acc tct aac gat att gct tta cgt att gcg 145
 Val Ile Pro Val Pro Glu Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala
 35 40 45

cgc gtg tta aat aaa ccg tat cgt caa ggt ttt gtg aaa aat cgc tat 193
 Arg Val Leu Asn Lys Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr
 50 55 60

gta gga cgt acg ttt att atg ccg ggg cag gca ttg cga gtc agt tct 241
 Val Gly Arg Thr Phe Ile Met Pro Gly Gln Ala Leu Arg Val Ser Ser
 65 70 75 80

gtt aga cgt aaa ctc aat acc att gct tca gaa ttt aaa gat aag aat	289																																																																																																																										
Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn																																																																																																																											
85	90		95	gtg tta tta gtt gac gac tcg att gta cgt ggt acc acg tct gaa caa	337	Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln		100	105		110	att gtc gaa atg gcg aga gcg gca ggt gcg aag aaa att tat ttt gcc	385	Ile Val Glu Met Ala Arg Ala Ala Gly Ala Lvs Lys Ile Tyr Phe Ala		115	120		125	tct gct gca cca gaa att cgt tat cca aat gtg tat ggt att gat atg	433	Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met		130	135		140	cca acc aaa aat gaa ttg atc gct tat ggt cgt gat gta gat gaa att	481	Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile		145	150		155		160	gct aac tta att ggt gtg gat aaa ttg att ttc caa gat ttg gat gcg	529	Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala		165	170		175	tta act ggt tct gtg caa caa gaa aat cca agt att caa gac ttt gat	577	Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp		180	185		190	tgt tcg gtg ttt aca ggg gtt tat gtg acg ggc gat att aca cct gaa	625	Cys Ser Val Phe Thr Gly Val Tyr Val Thr Gly Asp Ile Thr Pro Glu		195	200		205	tat ctg ga	633	Tyr Leu		210		<210> 46		<211> 210		<212> PRT		<213> Pasteurella multocida		<400> 46		Asp Gly Val Ser Val Tyr Ala Ala Arg Val His Met Gly Gln Arg Leu		1	5		10		15	Gly Glu Lys Ile Ala Arg Glu Trp Ala Asp Val Asp Asp Ile Asp Val		20	25		30	Val Ile Pro Val Pro Glu Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala		35	40		45	Arg Val Leu Asn Lys Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr		50	55		60	Val Gly Arg Thr Phe Ile Met Pro Gly Gln Ala Leu Arg Val Ser Ser		65	70		75		80	Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn		85	90		95	Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln		100	105		110
	95																																																																																																																										
gtg tta tta gtt gac gac tcg att gta cgt ggt acc acg tct gaa caa	337																																																																																																																										
Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln																																																																																																																											
100	105		110	att gtc gaa atg gcg aga gcg gca ggt gcg aag aaa att tat ttt gcc	385	Ile Val Glu Met Ala Arg Ala Ala Gly Ala Lvs Lys Ile Tyr Phe Ala		115	120		125	tct gct gca cca gaa att cgt tat cca aat gtg tat ggt att gat atg	433	Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met		130	135		140	cca acc aaa aat gaa ttg atc gct tat ggt cgt gat gta gat gaa att	481	Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile		145	150		155		160	gct aac tta att ggt gtg gat aaa ttg att ttc caa gat ttg gat gcg	529	Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala		165	170		175	tta act ggt tct gtg caa caa gaa aat cca agt att caa gac ttt gat	577	Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp		180	185		190	tgt tcg gtg ttt aca ggg gtt tat gtg acg ggc gat att aca cct gaa	625	Cys Ser Val Phe Thr Gly Val Tyr Val Thr Gly Asp Ile Thr Pro Glu		195	200		205	tat ctg ga	633	Tyr Leu		210		<210> 46		<211> 210		<212> PRT		<213> Pasteurella multocida		<400> 46		Asp Gly Val Ser Val Tyr Ala Ala Arg Val His Met Gly Gln Arg Leu		1	5		10		15	Gly Glu Lys Ile Ala Arg Glu Trp Ala Asp Val Asp Asp Ile Asp Val		20	25		30	Val Ile Pro Val Pro Glu Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala		35	40		45	Arg Val Leu Asn Lys Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr		50	55		60	Val Gly Arg Thr Phe Ile Met Pro Gly Gln Ala Leu Arg Val Ser Ser		65	70		75		80	Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn		85	90		95	Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln		100	105		110								
	110																																																																																																																										
att gtc gaa atg gcg aga gcg gca ggt gcg aag aaa att tat ttt gcc	385																																																																																																																										
Ile Val Glu Met Ala Arg Ala Ala Gly Ala Lvs Lys Ile Tyr Phe Ala																																																																																																																											
115	120		125	tct gct gca cca gaa att cgt tat cca aat gtg tat ggt att gat atg	433	Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met		130	135		140	cca acc aaa aat gaa ttg atc gct tat ggt cgt gat gta gat gaa att	481	Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile		145	150		155		160	gct aac tta att ggt gtg gat aaa ttg att ttc caa gat ttg gat gcg	529	Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala		165	170		175	tta act ggt tct gtg caa caa gaa aat cca agt att caa gac ttt gat	577	Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp		180	185		190	tgt tcg gtg ttt aca ggg gtt tat gtg acg ggc gat att aca cct gaa	625	Cys Ser Val Phe Thr Gly Val Tyr Val Thr Gly Asp Ile Thr Pro Glu		195	200		205	tat ctg ga	633	Tyr Leu		210		<210> 46		<211> 210		<212> PRT		<213> Pasteurella multocida		<400> 46		Asp Gly Val Ser Val Tyr Ala Ala Arg Val His Met Gly Gln Arg Leu		1	5		10		15	Gly Glu Lys Ile Ala Arg Glu Trp Ala Asp Val Asp Asp Ile Asp Val		20	25		30	Val Ile Pro Val Pro Glu Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala		35	40		45	Arg Val Leu Asn Lys Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr		50	55		60	Val Gly Arg Thr Phe Ile Met Pro Gly Gln Ala Leu Arg Val Ser Ser		65	70		75		80	Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn		85	90		95	Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln		100	105		110																
	125																																																																																																																										
tct gct gca cca gaa att cgt tat cca aat gtg tat ggt att gat atg	433																																																																																																																										
Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met																																																																																																																											
130	135		140	cca acc aaa aat gaa ttg atc gct tat ggt cgt gat gta gat gaa att	481	Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile		145	150		155		160	gct aac tta att ggt gtg gat aaa ttg att ttc caa gat ttg gat gcg	529	Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala		165	170		175	tta act ggt tct gtg caa caa gaa aat cca agt att caa gac ttt gat	577	Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp		180	185		190	tgt tcg gtg ttt aca ggg gtt tat gtg acg ggc gat att aca cct gaa	625	Cys Ser Val Phe Thr Gly Val Tyr Val Thr Gly Asp Ile Thr Pro Glu		195	200		205	tat ctg ga	633	Tyr Leu		210		<210> 46		<211> 210		<212> PRT		<213> Pasteurella multocida		<400> 46		Asp Gly Val Ser Val Tyr Ala Ala Arg Val His Met Gly Gln Arg Leu		1	5		10		15	Gly Glu Lys Ile Ala Arg Glu Trp Ala Asp Val Asp Asp Ile Asp Val		20	25		30	Val Ile Pro Val Pro Glu Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala		35	40		45	Arg Val Leu Asn Lys Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr		50	55		60	Val Gly Arg Thr Phe Ile Met Pro Gly Gln Ala Leu Arg Val Ser Ser		65	70		75		80	Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn		85	90		95	Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln		100	105		110																								
	140																																																																																																																										
cca acc aaa aat gaa ttg atc gct tat ggt cgt gat gta gat gaa att	481																																																																																																																										
Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile																																																																																																																											
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 115 120 125

Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met
 130 135 140

Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile
 145 150 155 160

Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala
 165 170 175

Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp
 180 185 190

Cys Ser Val Phe Thr Gly Val Tyr Val Thr Gly Asp Ile Thr Pro Glu
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Ile	Ile	Phe	Arg	Asp	Val	Ile	Glu	Arg	Tyr	Gln	Asn	Glu	Val	Ser	Ile		
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Thr	Lys	Gly	Ala	Arg	Asn	Glu	Ile	Ile	Arg	Leu	Asn	Arg	Phe	Leu			
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aga	tat	gat	att	tct	aat	ctg	tat	att	cgt	gat	tta	aga	aaa	gaa	gat		192
Arg	Tyr	Asp	Ile	Ser	Asn	Leu	Tyr	Ile	Arg	Asp	Leu	Arg	Lys	Glu	Asp		
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Phe	Glu	Glu	Trp	Ile	Arg	Ile	Arg	Leu	Thr	Glu	Val	Ser	Asp	Ala	Ser		
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Val	Arg	Arg	Glu	Leu	Val	Thr	Ile	Ser	Ser	Val	Leu	Thr	Thr	Ala	Ile		
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Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu Asp Lys Leu Pro Ile			
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Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala Leu Ile Leu Lys Met			
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Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln Asn Glu Val Ser Ile
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Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg Leu Asn Arg Phe Leu
 35 40 45

Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp Leu Arg Lys Glu Asp
 50 55 60

Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu Val Ser Asp Ala Ser
 65 70 75 80

Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val Leu Thr Thr Ala Ile
 85 90 95

Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met Thr Gly Ile Glu Lys
 100 105 110

Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr Ser Glu Gln Asp Ile
 115 120 125

Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu Asp Lys Leu Pro Ile
 130 135 140

Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu Phe Ala Ile Glu Thr
 145 150 155 160

Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys Trp Asp Asn Val Phe
 165 170 175

Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr Lys Asn Gly His Ser
 180 185 190

Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala Leu Ile Leu Lys Met
 195 200 205

Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln Thr Thr Pro Glu Ser
 210 215 220

Leu Ser Thr Thr Phe Arg Val Leu Lys Glu Cys Gly Leu Glu His
 225 230 235 240

Leu His Phe His Asp Thr Arg Arg Glu Ala Leu Thr Arg Leu Ser Lys
 245 250 255

Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser Gly His Arg Asp Leu
 260 265 270

Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn Met Ser Glu Val Ala
 275 280 285

Asn Leu Leu Asp
 290

<210> 49
<211> 1618
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (2)..(1195)

<220>
<223> sopE

<400> 49

g ggc gat cta tgt ctg aaa ata tct aca tgg tgt caa agt cac aga atc 49
 Gly Asp Leu Cys Leu Lys Ile Ser Thr Trp Cys Gln Ser His Arg Ile
 1 5 10 15

aat caa gca att cgc aca att caa agt cta tca acc gca gtc atc ggt 97
 Asn Gln Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly
 20 25 30

att gtc tgt act gca aat gac gca gac aat gaa aca ttc cca ctc aat 145
 Ile Val Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn
 35 40 45

gaa ccc gtt ctc atc aca aac gtg gca gcg gca att ggc aag gct gga 193
 Glu Pro Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly
 50 55 60

aaa caa ggc acg ctt tca cgt gcg ctt gac ggg att tct gat gta gtc 241
 Lys Gln Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val
 65 70 75 80

aat tgc aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac 289
 Asn Cys Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp
 85 90 95

gaa gaa aca aaa gca agt gaa atg aac acg gca att att ggc aca atc 337
 Glu Glu Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile
 100 105 110

aca gaa gaa ggg cag tac aca ggc ttg aag gcg tta ttg att gcg aaa 385
 Thr Glu Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys
 115 120 125

aac aaa ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac 433
 Asn Lys Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp
 130 135 140

aca aaa gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac 481
 Thr Lys Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn
 145 150 155 160

gca ttt gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg 529
 Ala Phe Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala
 165 170 175

gtg caa tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg 577
 Val Gln Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met
 180 185 190

ggc gat ttt ctg tca ttt aat gtc aac aca tca aaa gtt gag att gac 625
 Gly Asp Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp
 195 200 205

tat gcc gtc act cgt gcg gca atg cgt gca tat ctt gat aaa gaa 673
 Tyr Ala Val Thr Arg Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu
 210 215 220

cag ggc tgg cat acg tct att tca aat aaa ggc att aat ggc gtg agc 721
 Gln Gly Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser
 225 230 235 240

ggt gtc aca caa cca ctc tat ttt gac att aac gac agc tcg act gat	769
Gly Val Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp	
245	250
255	
gtg aac tat ctc aat gaa caa ggc atc acg tgt tgc gtg aat cat aat	817
Val Asn Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn	
260	265
270	
ggc ttt cgt ttt tgg ggc tta cgc acg act gca gaa gat cca tta ttc	865
Gly Phe Arg Phe Trp Gly Leu Arg Thr Ala Glu Asp Pro Leu Phe	
275	280
285	
aag ttt gaa gtg tac acc cgc act gca caa atc tta aaa gat acg att	913
Lys Phe Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile	
290	295
300	
gca ggg gcg ttt gat tgg gca gtg gat aaa gat att tct gtc acg cta	961
Ala Gly Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu	
305	310
315	320
gtg aaa gat att att gaa gca atc aat gcg aag tgg cgt gat tac acc	1009
Val Lys Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr	
325	330
335	
aca aaa ggc tac tta att ggc ggt aaa gcg tgg ctt aat aaa gag ctt	1057
Thr Lys Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu	
340	345
350	
aac agt gca acg aat tta aaa gat gcg aag ttg ttg atc tct tat gat	1105
Asn Ser Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp	
355	360
365	
tat cac cca gta cca ccg ctc gaa cag cta ggc ttt aat cag tac att	1153
Tyr His Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile	
370	375
380	
tct gat gaa tac ctt gtt gat ttt tca aat cgt tta gca tcg	1195
Ser Asp Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser	
385	390
395	
taagggttag aaaatggctt taccacgcaa acttaaatgg atgaatttaa tcatcgacgg	1255
taacaaatat ctcggcgaag tcacggaagt gactcaacca aaattagcaa tgaaaatcga	1315
agaatttcgc gcgggcggta tgattggttc ggtggatgtc aatctcgcc ttgaaaagct	1375
cgaagcggaa tttaaagccg gtggctacat ggtcgaatta attaaaaat tcggcgggtc	1435
aatcaacggc attccattgc gtttcttgg ctcatatcag cgtgatgaca cagaagaagt	1495
cacatctgtt gagcttgta tgcaaggctcg atttactgaa attgacagcgt gaaacagcaa	1555
agtggcgtat gacactgaac aaacattcaa agtgccctta acgtattaca aaatcattgt	1615
tga	1618

<210> 50
<211> 398
<212> PRT
<213> Pasteurella multocida

<400> 50

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 Asn Gln Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly
 20 25 30
 Ile Val Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn
 35 40 45
 Glu Pro Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly
 50 55 60
 Lys Gln Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val
 65 70 75 80
 Asn Cys Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp
 85 90 95
 Glu Glu Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile
 100 105 110
 Thr Glu Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys
 115 120 125
 Asn Lys Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp
 130 135 140
 Thr Lys Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn
 145 150 155 160
 Ala Phe Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala
 165 170 175
 Val Gln Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met
 180 185 190
 Gly Asp Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp
 195 200 205
 Tyr Ala Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu
 210 215 220
 Gln Gly Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser
 225 230 235 240
 Gly Val Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp
 245 250 255
 Val Asn Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn
 260 265 270
 Gly Phe Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe
 275 280 285
 Lys Phe Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile
 290 295 300
 Ala Gly Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu
 305 310 315 320
 Val Lys Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr
 325 330 335

Thr Lys Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu
 340 345 350

Asn Ser Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp
 355 360 365

Tyr His Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile
 370 375 380

Ser Asp Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
 385 390 395

<210> 51

<211> 353

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (1)..(351)

<220>

<223> unknown C1

<400> 51

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 Met Thr Leu Phe Asp Glu Cys Lys Leu Ala Leu Arg Asp Asp Phe Asn
 1 5 10 15

cta att tgt gat gaa gag aag gat tgt gta atg gat aag ttt tat ttc 96
 Leu Ile Cys Asp Glu Glu Lys Asp Cys Val Met Asp Lys Phe Tyr Phe
 20 25 30

tat ttc ttg gaa aag aaa gag gaa ttt aat ttt caa gat tat tca ttt 144
 Tyr Phe Leu Glu Lys Glu Phe Asn Phe Gln Asp Tyr Ser Phe
 35 40 45

gaa gaa atg tat ata ttt tca aaa atg gaa cct gtg tat gtt tta tgt 192
 Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys
 50 55 60

gat agc tct aat ata cct ttg ttt agg agt aat tgg gaa ttg att atc 240
 Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile
 65 70 75 80

aat aat ata tat gat gtt gtc tgt tta tct aca aaa gta ttt ttt cta 288
 Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu
 85 90 95

gat gat gaa aag tta atg atg gaa tta ttt cct gaa gat aaa gta aga 336
 Asp Asp Glu Lys Leu Met Met Glu Leu Phe Pro Glu Asp Lys Val Arg
 100 105 110

gtc atc tat aaa aga ta 353
 Val Ile Tyr Lys Arg
 115

<210> 52

<211> 117

<212> PRT

<213> Pasteurella multocida

<400> 52
Met Thr Leu Phe Asp Glu Cys Lys Leu Ala Leu Arg Asp Asp Phe Asn
1 5 10 15
Leu Ile Cys Asp Glu Glu Lys Asp Cys Val Met Asp Lys Phe Tyr Phe
20 25 30
Tyr Phe Leu Glu Lys Glu Glu Phe Asn Phe Gln Asp Tyr Ser Phe
35 40 45
Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys
50 55 60
Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile
65 70 75 80
Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu
85 90 95
Asp Asp Glu Lys Leu Met Met Glu Leu Phe Pro Glu Asp Lys Val Arg
100 105 110
Val Ile Tyr Lys Arg
115

<210> 53
<211> 509
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (1)..(507)

<220>
<223> unknown C2

<400> 53
atg aaa aat ttt agg aat ata aat att tat agt gat tat gga aag gtt 48
Met Lys Asn Phe Arg Asn Ile Asn Ile Tyr Ser Asp Tyr Gly Lys Val
1 5 10 15
gat aag gaa att ata tta gaa ttc gaa aat gaa ttt aat ata aag ctt 96
Asp Lys Glu Ile Ile Leu Glu Phe Glu Asn Glu Phe Asn Ile Lys Leu
20 25 30
cct tct tta tac ata gat tta att acg gcg cat aat gct ccg aag agt 144
Pro Ser Leu Tyr Ile Asp Leu Ile Thr Ala His Asn Ala Pro Lys Ser
35 40 45
gaa gag aat tgc ttt gaa tat tac aat gag cgt aat gag ccc acg ttt 192
Glu Glu Asn Cys Phe Glu Tyr Tyr Asn Glu Arg Asn Glu Pro Thr Phe
50 55 60
tct tcc ttt gga ttt gaa ggg ttt gag aca gag cgg tct agc gcc tct 240
Ser Ser Phe Gly Phe Glu Gly Phe Glu Thr Glu Arg Ser Ser Ala Ser
65 70 75 80
ctt gaa aat ata tat gct cag tat att tat gat gat cca atc tat ggt 288
Leu Glu Asn Ile Tyr Ala Gln Tyr Ile Tyr Asp Asp Pro Ile Tyr Gly
85 90 95

tat gaa cat gtg tat tct ttt ggt agt act ggc gag gga cat ttt atc 336
 Tyr Glu His Val Tyr Ser Phe Gly Ser Thr Gly Glu Gly His Phe Ile
 100 105 110

tgt ttt gat tat cgt gat gat cca aaa ggt gat gaa ccc aaa atc tgt 384
 Cys Phe Asp Tyr Arg Asp Asp Pro Lys Gly Asp Glu Pro Lys Ile Cys
 115 120 125

atc gtg att cac gat gaa tat gat gaa aaa aca ggg aaa atg cga ctg 432
 Ile Val Ile His Asp Glu Tyr Asp Glu Lys Thr Gly Lys Met Arg Leu
 130 135 140

ttt cct ata gca gag aat ttt gaa gcg ttt tta gat agt ttg aaa tca 480
 Phe Pro Ile Ala Glu Asn Phe Glu Ala Phe Leu Asp Ser Leu Lys Ser
 145 150 155 160

ttt gat gaa atg ata gag aag tat tcg ta 509
 Phe Asp Glu Met Ile Glu Lys Tyr Ser
 165

<210> 54

<211> 169

<212> PRT

<213> Pasteurella multocida

<400> 54

Met Lys Asn Phe Arg Asn Ile Asn Ile Tyr Ser Asp Tyr Gly Lys Val
 1 5 10 15

Asp Lys Glu Ile Ile Leu Glu Phe Glu Asn Glu Phe Asn Ile Lys Leu
 20 25 30

Pro Ser Leu Tyr Ile Asp Leu Ile Thr Ala His Asn Ala Pro Lys Ser
 35 40 45

Glu Glu Asn Cys Phe Glu Tyr Tyr Asn Glu Arg Asn Glu Pro Thr Phe
 50 55 60

Ser Ser Phe Gly Phe Glu Gly Phe Glu Thr Glu Arg Ser Ser Ala Ser
 65 70 75 80

Leu Glu Asn Ile Tyr Ala Gln Tyr Ile Tyr Asp Asp Pro Ile Tyr Gly
 85 90 95

Tyr Glu His Val Tyr Ser Phe Gly Ser Thr Gly Glu Gly His Phe Ile
 100 105 110

Cys Phe Asp Tyr Arg Asp Asp Pro Lys Gly Asp Glu Pro Lys Ile Cys
 115 120 125

Ile Val Ile His Asp Glu Tyr Asp Glu Lys Thr Gly Lys Met Arg Leu
 130 135 140

Phe Pro Ile Ala Glu Asn Phe Glu Ala Phe Leu Asp Ser Leu Lys Ser
 145 150 155 160

Phe Asp Glu Met Ile Glu Lys Tyr Ser
 165

<210> 55

<211> 443

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (1)...(441)

<220>

<223> unknown C3

<400> 55

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Met	Ile	Lys	Tyr	Leu	Glu	Gly	Asn	Ile	Asn	Ser	Phe	Ile	Ser	Ala	Leu	
1	5				10				15							

ggt	aaa	aac	gaa	agt	aat	aaa	gat	att	tta	aaa	tta	gta	gaa	ata	gtt	96
Gly	Lys	Asn	Glu	Ser	Asn	Lys	Lys	Asp	Ile	Leu	Lys	Leu	Val	Glu	Ile	Val
20	25				30											

tct	tca	gat	ttt	gaa	gtg	gat	gaa	cta	agt	cat	aaa	gat	gaa	cac	gag	144
Ser	Ser	Asp	Phe	Glu	Val	Asp	Glu	Leu	Ser	His	Lys	Asp	Glu	His	Glu	
35		40		45												

ata	tat	tat	ttg	ttt	tat	aag	agg	ggg	gtt	gaa	ttt	tgt	ttt	aaa	aga	192
Ile	Tyr	Tyr	Leu	Phe	Tyr	Lys	Arg	Gly	Val	Glu	Phe	Cys	Phe	Lys	Arg	
50		55		60												

ata	gat	gaa	gag	tat	gtc	tta	tat	tcg	gtt	tcc	ttt	ttg	gta	gag	240
Ile	Asp	Glu	Tyr	Val	Leu	Tyr	Ser	Val	Phe	Phe	Phe	Leu	Val	Glu	
65		70		75				80							

gtt	gat	aat	tat	ttt	tca	tgc	cca	ttt	att	cat	gaa	tta	ata	tgt	gat	288
Val	Asp	Asn	Tyr	Phe	Ser	Cys	Pro	Phe	Ile	His	Glu	Leu	Ile	Cys	Asp	
85		90		95												

ctt	aaa	cac	gga	ttc	tca	ata	gag	gat	att	ata	agg	ttt	tta	ggg	gag	336
Leu	Lys	His	Gly	Phe	Ser	Ile	Glu	Asp	Ile	Ile	Arg	Phe	Leu	Gly	Glu	
100		105		110												

cca	aat	ttt	aaa	ggg	agt	ggc	tgg	gta	aga	tat	tct	tat	aat	gga	aga	384
Pro	Asn	Phe	Lys	Gly	Ser	Gly	Trp	Val	Arg	Tyr	Ser	Tyr	Asn	Gly	Arg	
115		120		125												

aat	att	cat	ttc	gaa	ttt	aat	gaa	tct	aat	gaa	tta	tcc	cag	att	agc	432
Asn	Ile	His	Phe	Glu	Asn	Glu	Ser	Asn	Glu	Leu	Ser	Gln	Ile	Ser		
130		135		140												

att	ttt	att	ta													443
Ile	Phe	Ile														
145																

<210> 56

<211> 147

<212> PRT

<213> Pasteurella multocida

<400> 56

Met	Ile	Lys	Tyr	Leu	Glu	Gly	Asn	Ile	Asn	Ser	Phe	Ile	Ser	Ala	Leu	48
1	5				10			15								

Gly	Lys	Asn	Glu	Ser	Asn	Lys	Asp	Ile	Leu	Lys	Leu	Val	Glu	Ile	Val	96
20	25				30											

Ser Ser Asp Phe Glu Val Asp Glu Leu Ser His Lys Asp Glu His Glu
 35 40 45
 Ile Tyr Tyr Leu Phe Tyr Lys Arg Gly Val Glu Phe Cys Phe Lys Arg
 50 55 60
 Ile Asp Glu Glu Tyr Val Leu Tyr Ser Val Phe Phe Leu Val Glu
 65 70 75 80
 Val Asp Asn Tyr Phe Ser Cys Pro Phe Ile His Glu Leu Ile Cys Asp
 85 90 95
 Leu Lys His Gly Phe Ser Ile Glu Asp Ile Ile Arg Phe Leu Gly Glu
 100 105 110
 Pro Asn Phe Lys Gly Ser Gly Trp Val Arg Tyr Ser Tyr Asn Gly Arg
 115 120 125
 Asn Ile His Phe Glu Phe Asn Glu Ser Asn Glu Leu Ser Gln Ile Ser
 130 135 140
 Ile Phe Ile
 145

<210> 57
 <211> 8498
 <212> DNA
 <213> Pasteurella multocida

<220>
 <223> unknown C

<400> 57
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 aaaagtgtgg tacaacttaa accagaagag gtggaatggt catcaatcca ttatcctttc 180
 tttgtggcg atattcagca agtcgctcat ctcgcgaaag ccgcagaaat gggttgcgtg 240
 gtgattgata tgaaaggat ttgtgccagc ttgcaagacg tccctgtggt gataccggga 300
 gtaaatcagg aaaaatttgtt agatttacgt cagcgtataa ttgtgtcctt agccgatcca 360
 caagtgacac aacttgcatt agtcatcgcc tcgttgatgt caaatcacga aatcaaagac 420
 attgccgtaa cctcgttatt acctgcattct tatactaacg gagaaacggt aggtaaatta 480
 gcgggacaaa cagcgcgatt gttaaatggc attccacttg atgaaggcga acaacgtta 540
 gctttgatg tttccctac gcctgcattcg catttaataa tgcaaattca caagatctt 600
 ccacaattag ataatgtcgt atttcattct atccaagtgc ctgtttctt cgggatgggg 660
 caaatggta gcgtattatc ggattatgca ttagatcctc aatcttgctt agcgagctgg 720
 actgacaatc cggtgatgac ttatcatgca gaaaaatatt gcacccagt gacgaatggc 780
 gaacagggaaa tggcagaaga gcaaggcagca aaattacata taagtgggtt aagtgcgggtg 840
 gaaaatggtc tacaatttg gtcgggtgca gatgaacagc gcttaatct tgctttattg 900

agtgttacgc ttgcagagtt aatttactcg caaggttatt aatttaaatg tgaaaaatggca 960
cgatattttt atcttgaact ttgagagcgc actcgaaaa gacgagtgcg tttttgttaa 1020
aacattcgaa tgaaagacag tgaatgaata gcggagttat tgataagaat caatttatac 1080
aaaagcaact gaatgttatt aatcgaggca ataaacctat tgatagttt agttggcgcc 1140
ataatacata aactgtactt aataatatgc aatcaataacc tagaaatatt catgacgtaa 1200
tccaaacatat cggggagggg attttaagtg atggtagaaa aaacattttag aaatctaaaa 1260
atatatgatg attatggttc tgtctctcag gaaatttattt ttaatttga aaaagagttt 1320
gatataaaac tccctttatc ctatactca ctgtgaaaa agtataatgg cgtttggttt 1380
aaggaaagtg attttgaata tttatctcaa aatgggaaaa gaataataag ctcattgagt 1440
tttgatagtt ttgagacaaa agataatatac gaaccaatga ataataatatt aagacaatat 1500
atttatgatg atgaaattta tggatataag aatgtttattt cctttggtaa cactggaaat 1560
ggtgactttt tctgttttga ttatcgttat gacccaaaag gtgtgagcc caaaatctgt 1620
atcgtgattc atgatgaata tgatggaaaa acaggcaagc gtttggattt gcctgtggca 1680
gaaaattttt aggcattttt agatatgctt tacgattttt atgaacgcta tccgaatgg 1740
tatgaatagg tatttggtaa aataatgtgt tgtatTTTTT aagcatttatt tacaactaac 1800
attttaaagtg cggtaattt tgaaaaagtt ttggggctttt agaattgggc gcattttttt 1860
tgaaatattc ttcaatgatg agcactaattt atggattaga taatggaaat tatcgagata 1920
tggatggtaa taaaggatgg aggctagatt ttgatcctga gaaagttgtt catgtaaata 1980
ttttgactt tactaaaggt aaaggactag gtaaagcagt taaaaagtca ttcttttga 2040
tagtactgaa caagagttt aaaaattttt aagcaattaa ataaggaaga taaaatgaca 2100
ttatttggatg aatgtaaattt agctttttaga gacgatttttta atctaatttgg tcatgttgg 2160
aaggatttgtt taatggataa gttttatttc tatttttttgg aaaaagaaaga ggaatttaat 2220
tttcaagattt attcatttga agaaatgtat atattttcaaa aaatggaaacc tttgtatgtt 2280
ttatgtgata gctctaataat accttttttgg aggagtaattt gggaaattttagt tatcaataat 2340
atatatgatg ttgtctgtttt atctacaaaaa gtatttttttgc tagatgtatgaa aagttttaatg 2400
atggaatttat ttccctgaaga taaagtaaga gtcatctataa aaagataattt accccttgat 2460
cgcgcctcggt tcagcacgag ttcccttca ttaaagctct cgttaaagac tagcaactggc 2520
agtggggttt atcgtaatca atttactgaa gaacagttaa ttaaaaattaa taagaggctt 2580
gataaaaatag agggattttac atggcatcat aactcacaaaa gtagtccccca aaatatgttag 2640
ttaataccta caccaattca taaggctgtt cagcatatag gtgaaggcgc tttaagtgaa 2700
ggaaagtgtat aaaaatgaaaaa atttttaggaa tataaatattt tataatgttattt atgaaaggtt 2760
tgataaggaa attatatttag aattcgaaaaa tgaatttaat ataaagcttc cttctttata 2820

catagattta attacggcgc ataatgctcc gaagagtcaa gagaattgtt ttgaatatta 2880
caatgagcgt aatgagccca cgttttcttc ctttgattt gaagggttt agacagagcg 2940
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Pro Ile Thr Ile Asp Lys Pro Phe His Tyr Ser Cys Glu Glu Leu Asp			
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Ile Gln Gly Ile Ala Lys Leu Tyr Leu Arg Ser Glu Asn Ala Asn Ala		
115	120	125
Ser Ser Asp Ala Pro Ile Thr Ile Asp Lys Pro Phe His Tyr Ser Cys		
130	135	140
Glu Glu Leu Asp Leu Pro Thr Ala Asn Glu Tyr Ala Arg Arg Lys Pro		
145	150	155
Ile Val Cys Glu Val Gln Gly Gly Val Asn Arg Lys Phe Trp Leu Pro		
165	170	175
Val Ser Glu Ser Leu Val Ser Glu Asp Lys Leu Lys Lys Asp Arg Val		
180	185	190
Arg Leu Glu Ser Asp Thr Ser Tyr Ala Ile Lys Glu Lys Gly Ile Val		
195	200	205
Ile Pro Val Glu Leu Met Leu Val Ser Asp Tyr Ser Gly Ser Met Asn		
210	215	220
Ser His Leu Gln Asp Lys Asn Gly Arg Ser Leu Gly Lys Ala Lys Ile		
225	230	235
Thr Ile Leu Arg Glu Val Val Ser Glu Ile Ser Lys Ile Leu Leu Pro		
245	250	255
Glu Asp Val Ser Glu Gly Val Ser Pro Phe Asn Arg Ile Gly Phe Thr		
260	265	270
Thr Phe Ser Gly Gly Val Arg Gln Arg Asp Val Thr Glu Gly Cys Val		
275	280	285
Leu Pro Tyr Glu Gly Lys Ile Ser Gln Thr Ser Arg Lys Leu Thr Ile		
290	295	300
Arg Tyr Trp Ile Thr Gly Asn Asn Thr Pro Trp Lys Phe Asn Ala Gly		
305	310	315
Arg Trp Glu Arg Ser Thr Val Ser Phe Gln Glu His Tyr Lys Gly Tyr		
325	330	335
Tyr Asp Lys Phe His Ser Ser Thr Cys Arg Gly Ser Gly Ser Ser Arg		
340	345	350
Thr Cys Gln Ile Asp Ala Asn Pro Lys Lys Ile Met Asp Tyr Ala Leu		
355	360	365
Lys Ile Asn Asp Trp Thr Thr Ile Arg Glu Leu Phe Asn Thr Tyr Ile		
370	375	380
Asp Val Ser Gly Thr Ile Asp Gln Ile Ser Gln Phe Asp Gly Ser Asn		

385	390	395	400
Arg Arg Tyr Asp Met Val Phe Thr Asp Glu Glu Arg Cys Leu Gly Gly			
405		410	415
Asn Ile Gly Arg Arg Thr Thr Arg Ala Trp Phe Asp Gln Lys Asn Lys			
420		425	430
Asp Ile Thr Arg Glu Leu Asn Ile Val Arg Pro Ser Gly Trp Thr Ser			
435		440	445
Ala Ser Ser Gly Leu Leu Val Gly Ala Asn Ile Met Met Asp Glu Asn			
450		455	460
Lys Asn Pro Asp Ala Gln Pro Ser Lys Leu Gly Thr Asn Ile Gln Arg			
465		470	475
Val Ile Leu Val Leu Ser Asp Gly Glu Asp Asn Trp Pro Thr Tyr Ser			
485		490	495
Thr Leu Thr Thr Leu Leu Asn Asn Gly Met Cys Asp Lys Ile Arg Glu			
500		505	510
Gln Leu Gly Lys Leu Gln Asp Pro Asn Leu Arg Glu Leu Pro Gly Arg			
515		520	525
Ile Ala Phe Val Ala Phe Gly Tyr Ser Pro Pro Ala Asn Gln Val Ala			
530		535	540
Ala Trp Lys Lys Cys Val Gly Asp Gln Tyr Tyr Thr Ala Tyr Ser Lys			
545		550	555
Glu Glu Leu Leu Asp Ser Phe Lys Gln Ile Ile Gly Phe Glu Glu Glu			
565		570	575
Val Gly Arg Ser Ser Ser His Lys Pro Lys Phe			
580		585	

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<212> DNA
<213> Pasteurella multocida

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<222> (698)..(1468)

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gttaaatgttc aaacagggat tagtattgat gcggcttaa aacaagtggc aatcgatttt 360

aagaaaactta atccagatct tacttatgtg atgttaagga ttatttagaaa atctgaacctt 420
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 ttaattctag caccaggtat aatgagggtt tttccaa atg ttt aaa ttt acc 715
 Met Phe Phe Lys Phe Thr
 1 5

aag aaa atc gtt ttt gtt agt tta gct tta tct gtc gtt ggt ttt tct 763
 Lys Lys Ile Val Phe Val Ser Ala Leu Ser Val Val Gly Cys Ser
 10 15 20

acc cat tct cag caa ggc atg aca cag aaa agt atg tca tct gaa aca 811
 Thr His Ser Gln Gln Gly Met Thr Gln Lys Ser Met Ser Ser Glu Thr
 25 30 35

ata acg gca aaa gag act tta tat gaa agt acg caa aat tat tcg gca 859
 Ile Thr Ala Lys Glu Thr Leu Tyr Glu Ser Thr Gln Asn Tyr Ser Ala
 40 45 50

ctc att tca ctg tat cgc gat gtg ttg aaa gcc aaa gaa gat cct tca 907
 Leu Ile Ser Leu Tyr Arg Asp Val Leu Lys Ala Lys Glu Asp Pro Ser
 55 60 65 70

ata cgc tat aaa tta gcg aag aca tac tat cag cga ggt gac agc aaa 955
 Ile Arg Tyr Lys Leu Ala Lys Thr Tyr Tyr Gln Arg Gly Asp Ser Lys
 75 80 85

tct tct tta ctt tat tta acg cca tta ctg aat gat aat acg aag ctt 1003
 Ser Ser Leu Leu Tyr Leu Thr Pro Leu Leu Asn Asp Asn Thr Lys Leu
 90 95 100

gct aca caa gcg aaa ata tta cag ata aaa aat cta att caa tta aat 1051
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aat ttc caa gaa gca att tct gtc gca aat gaa ctc tta tta aaa tca 1099
 Asn Phe Gln Glu Ala Ile Ser Val Ala Asn Glu Leu Leu Lys Ser
 120 125 130

cct aat gaa gga gaa gta tat aat tta aga ggt atc gct tat gcg caa 1147
 Pro Asn Glu Gly Glu Val Tyr Asn Leu Arg Gly Ile Ala Tyr Ala Gln
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aat ggg aat ttg gtg aat gcc cga aat gat atc aat aaa gca aga gag 1195
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Tyr Leu Asn Gly Val Lys Asn Ser Arg Leu Ile His Asn Leu Val Phe
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 215 220 225 230

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 235 240 245

aaa act aca cat gta tca aaa ggt gta act cg^g taacactaag gatttgat 1488
 Lys Thr Thr His Val Ser Lys Gly Val Thr Arg
 250 255

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<210> 61

<211> 257

<212> PRT

<213> Pasteurella multocida

<400> 61

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Ser	Val	Val	Gly	Cys	Ser	Thr	His	Ser	Gln	Gln	Gly	Met	Thr	Gln	Lys
															30
									20	25					

Ser	Met	Ser	Ser	Glu	Thr	Ile	Thr	Ala	Lys	Glu	Thr	Leu	Tyr	Glu	Ser
															45
									35	40					

Thr	Gln	Asn	Tyr	Ser	Ala	Leu	Ile	Ser	Leu	Tyr	Arg	Asp	Val	Leu	Lys
															60
									50	55					

Ala	Lys	Glu	Asp	Pro	Ser	Ile	Arg	Tyr	Lys	Leu	Ala	Lys	Thr	Tyr	Tyr
															80
									65	70	75				

Gln	Arg	Gly	Asp	Ser	Lys	Ser	Ser	Leu	Leu	Tyr	Leu	Thr	Pro	Leu	Leu
															95
									85	90					

Asn	Asp	Asn	Thr	Lys	Leu	Ala	Thr	Gln	Ala	Lys	Ile	Leu	Gln	Ile	Lys
															110
									100	105					

Asn	Leu	Ile	Gln	Leu	Asn	Asn	Phe	Gln	Glu	Ala	Ile	Ser	Val	Ala	Asn
															125
									115	120					

Glu Leu Leu Leu Lys Ser Pro Asn Glu Gly Glu Val Tyr Asn Leu Arg
 130 135 140

Gly Ile Ala Tyr Ala Gln Asn Gly Asn Leu Val Asn Ala Arg Asn Asp
 145 150 155 160

Ile Asn Lys Ala Arg Glu Phe Phe Ile Asn Asp Asn Val Ala Ile Asn
 165 170 175

Asn Leu Ala Met Leu Asn Ile Ile Asn Gly Asp Phe Asn Asn Ala Val
 180 185 190

Ser Leu Leu Leu Pro Gln Tyr Leu Asn Gly Val Lys Asn Ser Arg Leu
 195 200 205

Ile His Asn Leu Val Phe Ala Leu Val Lys Asn Gly Asp Leu Asp Tyr
 210 215 220

Ala Lys Asp Ile Ile Val Lys Glu Arg Leu Asn Thr Ser Pro Asp Asp
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Leu Ile Asn Ala Leu Lys Lys Thr Thr His Val Ser Lys Gly Val Thr
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Arg

<210> 62

<211> 1788

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (1)..(600)

<220>

<223> unknown K

<400> 62

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aaa gat gac acc agt ttt gtg act gaa gga aat aac ttt atc aca gca 96
 Lys Asp Asp Thr Ser Phe Val Thr Glu Gly Asn Asn Phe Ile Thr Ala
 20 25 30

aaa gac aac tta gaa atc acg gca aaa aat gtt caa att gat caa gcg 144
 Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn Val Gln Ile Asp Gln Ala
 35 40 45

aaa aat att caa tta aac gcg aat atc acg atc aat acc aag tct ggt 192
 Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr Ile Asn Thr Lys Ser Gly
 50 55 60

ttt gtg aat tac ggt acc tta gca agt gct caa aat tta acg att aat 240
 Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala Gln Asn Leu Thr Ile Asn
 65 70 75 80

acc gaa caa ggc agc att tat aac ata ggc ggt atc ttg ggg gcg ggt 288
 Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly Gly Ile Leu Gly Ala Gly

85	90	95	
aaa agt ttg aat ctg agc gcg aaa aga gga gaa aac caa gga gga tat Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly Glu Asn Gln Gly Gly Tyr 100	105	110	336
ctt att aat caa ggt aag agt cta ctc cat tct gaa ggc gcc atg aac Leu Ile Asn Gln Gly Lys Ser Leu Leu His Ser Glu Gly Ala Met Asn 115	120	125	384
ctc aca gcg gat cgc acg gty tac aat tta ggg aat att ttt gct aaa Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu Gly Asn Ile Phe Ala Lys 130	135	140	432
ggt gac gcg acg atc aat gca aac gcg tta att aat gat gtt act ctc Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu Ile Asn Asp Val Thr Leu 145	150	155	480
aca ggt cgt ctt gag tat caa gat ctg aaa aaa gat tat acg cgt tat Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys Lys Asp Tyr Thr Arg Tyr 165	170	175	528
tat cgt atc aat gaa acg gca aaa cat ggt tgg cat aat aac ttc tat Tyr Arg Ile Asn Glu Thr Ala Lys His Gly Trp His Asn Asn Phe Tyr 180	185	190	576
gaa tta aac gtc gac aga gtt tct tgatttgtc atcaattttg taaccaccgg Glu Leu Asn Val Asp Arg Val Ser 195	200		630
ttaataaaac accagcaatt tcaacgccat tcatggcaga taatgccgct gcgacgatca catcaggacg atccgcggaa gtgacaagta aacttccaac gcggaaatgt tccaccatat tggtaaaatt acgtgcacag aaagtgtatgc cacgaatgcg acgttcattt atcgccctt catgaataat ggcagcacct aaatgtttgg ctaaatcaat ggcacgagtc gcaattaatt ctgcgctcca aggaatacat gccaagattt taattggct tttctcaat aaatgataaa tctcagatac ttgattttgt gtgtgttgga aagaatcaaa aatttctgcc aagtcaggc gagttacgacc agattcatca atcggcgcat taaatttatt gatcacaaca ccaagtaaat tagggttatt tttgctgcca aataatgagg ctgcggcttt gatgcgttct ttgagttctg ccgggttttc cgtegcgggt gctgcaacaa gaatgatttc cgcatcaagt gcttgagca tttcatagtt aatgctattt gcataagaat gcttacgcgt agggattaaa cttccacca cgacaatttc attgtttttg gcgagttgtt gatgattttc aacaattttt tctagtagcca catcagattt atttgaccg atgagtgatt cagctacact taacataaaat ggttcactgg tttcaatggt ggtactggtg cgaataattt atgttgcgt atcaatcata tcttcaccc agttcggctg agaaatttggt ttcataaaagc cgactttcgc cccttttgc tccagtgcat gtgttaaacc taagctgaca ctggtaaagc ctacaccagc actaatcggg ataaggataa ttgtacgtga cataataaaac cctaatttgc tgataatttata tacaaaaaga aactgccc gaatcggcag ttaatttgc tttacgcgt qcaaaaggcgc qcggtatctt qtqcaataac 1650			

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 <211> 200
 <212> PRT
 <213> Pasteurella multocida

<400> 63
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Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn Val Gln Ile Asp Gln Ala
 35 40 45

Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr Ile Asn Thr Lys Ser Gly
 50 55 60

Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala Gln Asn Leu Thr Ile Asn
 65 70 75 80

Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly Gly Ile Leu Gly Ala Gly
 85 90 95

Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly Glu Asn Gln Gly Gly Tyr
 100 105 110

Leu Ile Asn Gln Gly Lys Ser Leu Leu His Ser Glu Gly Ala Met Asn
 115 120 125

Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu Gly Asn Ile Phe Ala Lys
 130 135 140

Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu Ile Asn Asp Val Thr Leu
 145 150 155 160

Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys Lys Asp Tyr Thr Arg Tyr
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Tyr Arg Ile Asn Glu Thr Ala Lys His Gly Trp His Asn Asn Phe Tyr
 180 185 190

Glu Leu Asn Val Asp Arg Val Ser
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<210> 64
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 <212> DNA
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<220>
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<223> unknown O

<400> 64

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Met Lys Ile
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Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser Ala Arg Leu
5 10 15

gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca tta aca ttg 212
Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala Leu Thr Leu
20 25 30 35

gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt gag gag gaa 260
Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly Glu Glu Glu
40 45 50

agc aaa agg gga cat agt 278
Ser Lys Arg Gly His Ser
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<210> 65

<211> 57

<212> PRT

<213> Pasteurella multocida

<400> 65

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Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
35 40 45

Glu Glu Glu Ser Lys Arg Gly His Ser
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<210> 66

<211> 1020

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (1)...(597)

<220>

<223> unknown P

<400> 66

gtc aac aca tca aaa gtt gag att gac tat gcc gtc act cgt gcg gcg 48
Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala Val Thr Arg Ala Ala
1 5 10 15

gca atg cgt gca tat ctt gat aaa gaa cag ggc tgg cat acg tct att 96

Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile			
20	25	30	
tca aat aaa ggc att aat ggc gtg agc ggt gtc aca caa cca ctc tat		144	
Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr			
35	40	45	
ttt gac att aac gac agc tcg act gat gtg aac tat ctc aat gaa caa		192	
Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln			
50	55	60	
ggc atc acg tgt tgc gtg aat cat aat ggc ttt cgt ttt tgg ggc tta		240	
Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu			
65	70	75	80
cgc acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc		288	
Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg			
85	90	95	
act gca caa atc tta aaa gat acg att gca ggg gcg ttt gat tgg gca		336	
Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala			
100	105	110	
gtg gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca		384	
Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala			
115	120	125	
atc aat gcg aag tgg cgt gat tac acc aca aaa ggc tac tta att ggc		432	
Ile Asn Ala Lys Trp Arg Asp Tyr Thr Lys Gly Tyr Leu Ile Gly			
130	135	140	
ggt aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa		480	
Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys			
145	150	155	160
gat gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc		528	
Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu			
165	170	175	
gaa cag cta ggc ttt aat cag tac att tct gat gaa tac ctt gtt gat		576	
Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp			
180	185	190	
ttt tca aat cgt tta gca tcg taagggtag aaaaatggctt taccacgcaa		627	
Phe Ser Asn Arg Leu Ala Ser			
195			
acttaaatttg atgaatttaa tcatcgacgg taacaaatat ctccggcgaag tcacggaagt		687	
gactcaacca aaatttagcaa tgaaaatcga agaatttcgc gcggggcgta tgatgggttc		747	
ggtgatgtc aatctcggtc ttgaaaagct cgaagcggaa tttaagccg gtggctacat		807	
ggtcgaatta attaaaaat tcggcggtc aatcaacggc attccattgc gttttcttgg		867	
ctcatatcag cgtgatgaca cagaagaagt cacatctgtt gagcttgtga tgcaaggcgt		927	
atttactgaa attgacagcg gaaacagcaa agtgggcgtat gacactgaac aaacattcaa		987	
agtgccttta acgtattaca aaatcattgt tga		1020	

<211> 199
<212> PRT
<213> Pasteurella multocida

<400> 67
Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala Val Thr Arg Ala Ala
1 5 10 15
Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile
20 25 30
Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr
35 40 45
Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln
50 55 60
Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu
65 70 75 80
Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg
85 90 95
Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala
100 105 110
Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala
115 120 125
Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly
130 135 140
Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys
145 150 155 160
Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu
165 170 175
Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp
180 185 190
Phe Ser Asn Arg Leu Ala Ser
195

<210> 68
<211> 2584
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (1042)..(2286)

<220>
<223> xylA

<400> 68
gtcgaccagc ttagattttg cgacgggtt aatttcttct atcgttcaa tcattgcgtt 60
taccattatt ttatggaatc tctctggacc gatgaccatt gccaatattg aaattcctca 120
cgcgatggtc ttttggctt ttatcacgt gctgttttagc agtattgtgg catttaaaat 180

cggtcgcccc ttaattcagc tcaattttgc caatgaacgc ttaaacgcc aactaccgtta 240
 ttcacttatac cgtctgaaag aatatgctga aagcattgct ttttatcggt gtgaaaaaat 300
 ggaaaaacgt ctattgacca cacaatttaa tcaggtgatt gataacgttt ggcaagtaat 360
 ctaccgcacc ttgaaattat ccggttttaa cttaatcatt acgcagattt cggtggttt 420
 tccgctggtg attcaagtga cacgttattt tcgtcgacaa taggtgcata tgagggtgtt 480
 agaatagcga tactttctgt tggaaaagta aactctttaa tataaataga aatcgcttga 540
 atgattctcg ggcaaaaaat aatgtactca tttgcgatct catactgata atggcgaagt 600
 aaatatcttc ttacaatattt atggtaattt tcaggttaata ccgtatagcc atagattcca 660
 gttctatttt gtttgctaa ataattgatg agcattttag ggcgcaggtaa atccatatct 720
 gcaacagaca ttgaaatcat atccttgcgg tatttacgag taattgccc tttagcacta 780
 tgacaatctg atctatcagt aaaaacatca aacaaattat ccgtcataca tgttctccaa 840
 tattggattt atataaaactt tagaacttga ggttagattgt tggaaattgtt aaatctggta 900
 tttcttattac gtttttctt ttttggtata taagccacaa taaccaataa tcttaattgt 960
 taagtgaaat aacgtaattt atcctccat tggttacta aattatgtct ctgaaactta 1020
 tttgttcagg agaaatcatt t atg tcc act tac ttc gac aaa att gaa aaa 1071
 Met Ser Thr Tyr Phe Asp Lys Ile Glu Lys
 1 5 10

 gta aat tat gaa ggt gta act tca tct aat ccg ttt gca tat aag cat 1119
 Val Asn Tyr Glu Gly Val Thr Ser Ser Asn Pro Phe Ala Tyr Lys His
 15 20 25

 tat gat gct aat caa gtt att tta ggt aag acg atg gct gaa cac tta 1167
 Tyr Asp Ala Asn Gln Val Ile Leu Gly Lys Thr Met Ala Glu His Leu
 30 35 40

 cgt tta gcc gtc tgt tat tgg cac act ttc tgt tgg aca ggg aat gat 1215
 Arg Leu Ala Val Cys Tyr Trp His Thr Phe Cys Trp Thr Gly Asn Asp
 45 50 55

 atg ttc ggt gtc ggt tct ttc gat cgt tgt tgg cag aag gcg agt gat 1263
 Met Phe Gly Val Gly Ser Phe Asp Arg Cys Trp Gln Lys Ala Ser Asp
 60 65 70

 tca tta gca ggt gca aaa caa aaa gca gat atc gct ttt gaa ttt ttc 1311
 Ser Leu Ala Gly Ala Lys Gln Lys Ala Asp Ile Ala Phe Glu Phe Phe
 75 80 85 90

 agt aaa tta ggc ata cct tat tat tgt ttt cat gat gtt gat gtt gcg 1359
 Ser Lys Leu Gly Ile Pro Tyr Tyr Cys Phe His Asp Val Asp Val Ala
 95 100 105

 cca gaa ggt cat tca ttt aaa gaa tat ttg tcg aac ttt aat aca atg 1407
 Pro Glu Gly His Ser Phe Lys Glu Tyr Leu Ser Asn Phe Asn Thr Met
 110 115 120

 atc gat gtt tta gcg cag aaa caa gaa gaa aca ggc gtc aaa ttg ttg 1455
 Ile Asp Val Leu Ala Gln Lys Gln Glu Glu Thr Gly Val Lys Leu Leu
 125 130 135

tgg	ggg	act	gca	aat	tgt	ttt	aca	cac	cct	cgt	tat	atg	tct	ggg	gct	1503
Trp	Gly	Thr	Ala	Asn	Cys	Phe	Thr	His	Pro	Arg	Tyr	Met	Ser	Gly	Ala	
140												150				
gca	aca	aat	ccg	aat	cca	gaa	att	ttt	gct	tgg	gct	gct	gca	caa	gta	1551
Ala	Thr	Asn	Pro	Asn	Pro	Glu	Ile	Phe	Ala	Trp	Ala	Ala	Ala	Gln	Val	
155												165			170	
ttt	act	gcc	atg	ggg	gca	act	cag	cgt	tta	ggt	ggt	gaa	aat	tat	gtt	1599
Phe	Thr	Ala	Met	Gly	Ala	Thr	Gln	Arg	Leu	Gly	Gly	Asn	Tyr	Val		
175												180		185		
ttg	tgg	gga	gga	cgt	gaa	gga	tat	gaa	acg	tta	tta	aat	acc	aat	tta	1647
Leu	Trp	Gly	Gly	Arg	Glu	Gly	Tyr	Glu	Thr	Leu	Leu	Asn	Thr	Asn	Leu	
190											195		200			
aaa	cag	gag	cga	gag	caa	att	gga	cgt	ttc	atg	caa	atg	gtg	gtt	gag	1695
Lys	Gln	Glu	Arg	Glu	Gln	Ile	Gly	Arg	Phe	Met	Gln	Met	Val	Val	Glu	
205											210		215			
cat	aaa	tat	aaa	atc	ggt	ttt	aac	ggg	act	ttg	ctg	att	gaa	cca	aag	1743
His	Lys	Tyr	Lys	Ile	Gly	Phe	Asn	Gly	Thr	Leu	Leu	Ile	Glu	Pro	Lys	
220											225		230			
cca	caa	gag	cca	acg	aaa	cat	caa	tat	gac	tat	gat	gtg	gcg	acc	gtt	1791
Pro	Gln	Glu	Pro	Thr	Lys	His	Gln	Tyr	Asp	Tyr	Asp	Val	Ala	Thr	Val	
235											240		245		250	
tat	ggc	ttt	tta	aag	cag	ttt	ggt	tta	gaa	aaa	gaa	att	aaa	gtg	aat	1839
Tyr	Gly	Phe	Leu	Lys	Gln	Phe	Gly	Leu	Glu	Lys	Glu	Ile	Lys	Val	Asn	
255											260		265			
att	gaa	gct	aat	cac	gca	aca	tta	gct	gga	cac	act	ttc	cag	cat	gaa	1887
Ile	Glu	Ala	Asn	His	Ala	Thr	Leu	Ala	Gly	His	Thr	Phe	Gln	His	Glu	
270											275		280			
gtc	gcc	atg	gct	aca	gcg	tta	gat	att	ttt	ggt	tct	att	gat	gca	aat	1935
Val	Ala	Met	Ala	Thr	Ala	Leu	Asp	Ile	Phe	Gly	Ser	Ile	Asp	Ala	Asn	
285											290		295			
cgt	ggt	gat	cca	caa	tta	ggt	tgg	gat	acc	gat	caa	ttc	cct	aat	agc	1983
Arg	Gly	Asp	Pro	Gln	Leu	Gly	Trp	Asp	Thr	Asp	Gln	Phe	Pro	Asn	Ser	
300											305		310			
gta	gaa	gaa	aat	act	ttg	gtc	ata	tat	gaa	att	ctc	aaa	gca	ggg	ggc	2031
Val	Glu	Glu	Asn	Thr	Leu	Val	Ile	Tyr	Glu	Ile	Leu	Lys	Ala	Gly	Gly	
315											320		325		330	
ttt	aca	acc	ggt	ttt	aat	ttt	gat	gct	aaa	atc	cgt	cg	cag	agt	2079	
Phe	Thr	Thr	Gly	Gly	Phe	Asn	Phe	Asp	Ala	Lys	Ile	Arg	Arg	Gln	Ser	
335											340		345			
acg	gat	cct	tac	gat	tta	ttt	cat	gga	cat	att	ggc	gcg	att	gat	gta	2127
Thr	Asp	Pro	Tyr	Asp	Leu	Phe	His	Gly	His	Ile	Gly	Ala	Ile	Asp	Val	
350											355		360			
ctt	gcc	tta	tca	cta	aaa	tgt	gcg	gcg	aaa	atg	ctt	gaa	gag	caa	gct	2175
Leu	Ala	Leu	Ser	Leu	Lys	Cys	Ala	Ala	Lys	Met	Leu	Glu	Gln	Ala		
365											370		375			
tta	caa	aaa	gtc	gtc	aat	caa	cgt	tat	gct	ggt	tgg	aca	tca	tca	ctt	2223
Leu	Gln	Lys	Val	Val	Asn	Gln	Arg	Tyr	Ala	Gly	Trp	Thr	Ser	Ser	Leu	
380											385		390			

ggt caa ctt gtt caa atc cgg tcc tac cac gcg tgt ctg caa tac aga 2271
 Gly Gln Leu Val Gln Ile Arg Ser Tyr His Ala Cys Leu Gln Tyr Arg
 395 400 405 410

cta aca aaa gtg ctt taaaacgttc cggttacgc cagacatcta gacgattgaa 2326
 Leu Thr Lys Val Leu
 415

taatttcaat attgtctccg cacgttaattc aaaggcttg tgtatgtgcg aatgatattc 2386
 acaacaaaagt tctgaaaaat cttgaattgc gtgaggtaat ttaaagcgct gacataagcg 2446
 tcttgcggc atgacaccag cttttcatg tccataatga tgtggcaata tttctttgg 2506
 tgttaaggct tttcctaaat catgacaaaat tgtagcaaaa cgtaccgcac ttttgtcact 2566
 gtccgtgttt tctgtcga 2584

<210> 69
<211> 415
<212> PRT
<213> Pasteurella multocida

<400> 69
Met Ser Thr Tyr Phe Asp Lys Ile Glu Lys Val Asn Tyr Glu Gly Val
1 5 10 15

Thr Ser Ser Asn Pro Phe Ala Tyr Lys His Tyr Asp Ala Asn Gln Val
20 25 30

Ile Leu Gly Lys Thr Met Ala Glu His Leu Arg Leu Ala Val Cys Tyr
35 40 45

Trp His Thr Phe Cys Trp Thr Gly Asn Asp Met Phe Gly Val Gly Ser
50 55 60

Phe Asp Arg Cys Trp Gln Lys Ala Ser Asp Ser Leu Ala Gly Ala Lys
65 70 75 80

Gln Lys Ala Asp Ile Ala Phe Glu Phe Phe Ser Lys Leu Gly Ile Pro
85 90 95

Tyr Tyr Cys Phe His Asp Val Asp Val Ala Pro Glu Gly His Ser Phe
100 105 110

Lys Glu Tyr Leu Ser Asn Phe Asn Thr Met Ile Asp Val Leu Ala Gln
115 120 125

Lys Gln Glu Glu Thr Gly Val Lys Leu Leu Trp Gly Thr Ala Asn Cys
130 135 140

Phe Thr His Pro Arg Tyr Met Ser Gly Ala Ala Thr Asn Pro Asn Pro
145 150 155 160

Glu Ile Phe Ala Trp Ala Ala Ala Gln Val Phe Thr Ala Met Gly Ala
165 170 175

Thr Gln Arg Leu Gly Gly Glu Asn Tyr Val Leu Trp Gly Gly Arg Glu
180 185 190

Gly Tyr Glu Thr Leu Leu Asn Thr Asn Leu Lys Gln Glu Arg Glu Gln
195 200 205

Ile Gly Arg Phe Met Gln Met Val Val Glu His Lys Tyr Lys Ile Gly
 210 215 220

Phe Asn Gly Thr Leu Leu Ile Glu Pro Lys Pro Gln Glu Pro Thr Lys
 225 230 235 240

His Gln Tyr Asp Tyr Asp Val Ala Thr Val Tyr Gly Phe Leu Lys Gln
 245 250 255

Phe Gly Leu Glu Lys Glu Ile Lys Val Asn Ile Glu Ala Asn His Ala
 260 265 270

Thr Leu Ala Gly His Thr Phe Gln His Glu Val Ala Met Ala Thr Ala
 275 280 285

Leu Asp Ile Phe Gly Ser Ile Asp Ala Asn Arg Gly Asp Pro Gln Leu
 290 295 300

Gly Trp Asp Thr Asp Gln Phe Pro Asn Ser Val Glu Glu Asn Thr Leu
 305 310 315 320

Val Ile Tyr Glu Ile Leu Lys Ala Gly Gly Phe Thr Thr Gly Gly Phe
 325 330 335

Asn Phe Asp Ala Lys Ile Arg Arg Gln Ser Thr Asp Pro Tyr Asp Leu
 340 345 350

Phe His Gly His Ile Gly Ala Ile Asp Val Leu Ala Leu Ser Leu Lys
 355 360 365

Cys Ala Ala Lys Met Leu Glu Glu Gln Ala Leu Gln Lys Val Val Asn
 370 375 380

Gln Arg Tyr Ala Gly Trp Thr Ser Ser Leu Gly Gln Leu Val Gln Ile
 385 390 395 400

Arg Ser Tyr His Ala Cys Leu Gln Tyr Arg Leu Thr Lys Val Leu
 405 410 415

<210> 70

<211> 3501

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (298)...(1905)

<220>

<223> yabk

<400> 70

gaattcgagg aagggggcgtt attacaaatt gaaacggctg cacgtgtac acaacatgtat 60

aatgcctgtg cggatcattt cttgccttt ttacttcatc cagaagcaca agggcattta 120

gtcaagaata atgtgatgtt accggtgatt aataccaata ttgaaccgca ctttgatgcc 180

ctttagagcca cccaaatgaa cacgaaagtg ctcgataacct caaaaagtgaa tgccgaacaa 240

gtcaaaaaat ggattgctgt ttggcaaacg accctaacc aataattgtt tgtcttg 297

atg ttt aag cga ttt cgt gca ttc aca tac cgt ccc gcc agt tat ctt	345
Met Phe Lys Arg Phe Arg Ala Phe Thr Tyr Arg Pro Ala Ser Tyr Leu	
1 5 10 15	
ggc ggg atg ttg gtg att gtt ttt ctg agc gct ttt tat gcg ttc gcc	393
Gly Gly Met Leu Val Ile Val Phe Leu Ser Ala Phe Tyr Ala Phe Ala	
20 25 30	
tta ggg gcg gtt ttt tcg ctc cct ttt gcg cgc agt tgg aca gcg ttg	441
Leu Gly Ala Val Phe Ser Leu Pro Phe Ala Arg Ser Trp Thr Ala Leu	
35 40 45	
ttg agt gat cag tat tta caa cac gtg atc atc ttt agc ttt tgg caa	489
Leu Ser Asp Gln Tyr Leu Gln His Val Ile Ile Phe Ser Phe Trp Gln	
50 55 60	
gcc ttt ctg tcg gcg gta ctt gcg gtc ctc ttt ggt ggc att gta gca	537
Ala Phe Leu Ser Ala Val Leu Ala Val Phe Gly Gly Ile Val Ala	
65 70 75 80	
cga gcc ttt ttt tat caa ccg ttt gtg ggc aag aaa ctg atc ctc aaa	585
Arg Ala Phe Phe Tyr Gln Pro Phe Val Gly Lys Lys Leu Ile Leu Lys	
85 90 95	
tta ttt tca ctg act ttt gtg tta cct gcc tta gtg gcg att ttt ggt	633
Leu Phe Ser Leu Thr Phe Val Leu Pro Ala Leu Val Ala Ile Phe Gly	
100 105 110	
tta tta ggc gtg tat ggc gct tct ggc tgg tta gcg atg tta agc cag	681
Leu Leu Gly Val Tyr Gly Ala Ser Gly Trp Leu Ala Met Leu Ser Gln	
115 120 125	
ttt ttc gct tgg gat tgg act cct aat att tac ggc tta aca ggt att	729
Phe Phe Ala Trp Asp Trp Thr Pro Asn Ile Tyr Gly Leu Thr Gly Ile	
130 135 140	
tta ctg gcg cat ctt ttt aat gtc cca tta gct tgt cgc ctg ttt	777
Leu Leu Ala His Leu Phe Phe Asn Val Pro Leu Ala Cys Arg Leu Phe	
145 150 155 160	
tta caa ggt ttg caa gca att ccg gtg caa caa cgt cag ctc gcg gca	825
Leu Gln Gly Leu Gln Ala Ile Pro Val Gln Gln Arg Gln Leu Ala Ala	
165 170 175	
caa ctc aat tta cgt ggt tgg cat ttt ata cgt ctg att gag tgg ccc	873
Gln Leu Asn Leu Arg Gly Trp His Phe Ile Arg Leu Ile Glu Trp Pro	
180 185 190	
tat tta cgc cag caa ttg tta cct gca ttt act ttg att ttc atg ctg	921
Tyr Leu Arg Gln Gln Leu Leu Pro Ala Phe Thr Leu Ile Phe Met Leu	
195 200 205	
tgt ttt acc agt ttt gcg att gtg ctc act tta ggt ggc gga ccg aaa	969
Cys Phe Thr Ser Phe Ala Ile Val Leu Thr Leu Gly Gly Gly Pro Lys	
210 215 220	
tat acc acg ttg gaa gtg gct atc tat caa gcg att tta ttt gag ttt	1017
Tyr Thr Thr Leu Glu Val Ala Ile Tyr Gln Ala Ile Leu Phe Glu Phe	
225 230 235 240	
gat gta ccg aaa gcc ggc tta ttt gcg tta tta caa ttt gtt ttt tgt	1065
Asp Val Pro Lys Ala Gly Leu Phe Ala Leu Leu Gln Phe Val Phe Cys	
245 250 255	

ttt ctg tta ttc acg ctg agt agc ttt ttc cca gcc ccc gcc acg Phe Leu Leu Phe Thr Leu Ser Ser Phe Phe Ser Pro Ala Pro Ala Thr 260 265 270	1113
aca tta cac agtcaa cct act tgg ttt gcg ccc caa tcg tat tgg gtt Thr Leu His Ser Gln Pro Thr Trp Phe Ala Pro Gln Ser Tyr Trp Val 275 280 285	1161
aaa tta tgg caa cgt atg atc att gtg tgt gcg aca gta ttt atc tta Lys Leu Trp Gln Arg Met Ile Ile Val Cys Ala Thr Val Phe Ile Leu 290 295 300	1209
tta ccg cta ctc aat acg cta gtt tct gct ttg ctt tcg tct cag ttt Leu Pro Leu Leu Asn Thr Leu Val Ser Ala Leu Leu Ser Ser Gln Phe 305 310 315 320	1257
ttt acc ttg tgg tta caa cct caa tta tgg aaa gca tta ggt tac tcg Phe Thr Leu Trp Leu Gln Pro Gln Leu Trp Lys Ala Leu Gly Tyr Ser 325 330 335	1305
ctc acc atc gcc ccc act tct gca ttg ctc gct tta gta ctg tct ttt Leu Thr Ile Ala Pro Thr Ser Ala Leu Leu Ala Leu Val Leu Ser Phe 340 345 350	1353
gcc tta tta ttg ctt gcc aga gaa tta cat tgg cga cat tat cgc agc Ala Leu Leu Leu Ala Arg Glu Leu His Trp Arg His Tyr Arg Ser 355 360 365	1401
tta tcc cat gtg att tta aat atc ggt gcg acc att tta gcc att cca Leu Ser His Val Ile Leu Asn Ile Gly Ala Thr Ile Leu Ala Ile Pro 370 375 380	1449
acg tta gtg tta gct att ggt tta ttc att tta tta cgt gag atc gat Thr Leu Val Leu Ala Ile Gly Leu Phe Ile Leu Leu Arg Glu Ile Asp 385 390 395 400	1497
ttt tct cca tac cat ctt ttt ggg gtt gtg gta tgc tgt aac gcg tta Phe Ser Pro Tyr His Leu Phe Gly Val Val Val Cys Cys Asn Ala Leu 405 410 415	1545
gct gct atg cct ttt gtg ttg cgt att ttg gct tta ccg atg cat aac Ala Ala Met Pro Phe Val Leu Arg Ile Leu Ala Leu Pro Met His Asn 420 425 430	1593
aat atg att tat tat gaa aaa tta tgc caa tca ctt aac ctg cgt ggt Asn Met Ile Tyr Tyr Glu Lys Leu Cys Gln Ser Leu Asn Leu Arg Gly 435 440 445	1641
tgg caa cgt ttt cga ttg att gaa tgg cac aag ctt cgt gcg cca atg Trp Gln Arg Phe Arg Leu Ile Glu Trp His Lys Leu Arg Ala Pro Met 450 455 460	1689
aaa tac gcc ttt gca ctg gct tgt gcg tta tca tta ggc gat ttc acc Lys Tyr Ala Phe Ala Leu Ala Cys Ala Leu Ser Leu Gly Asp Phe Thr 465 470 475 480	1737
gca atc gcg tta ttt ggt cag gct gac ttc aca tcg tta ccg cat ttg Ala Ile Ala Leu Phe Gly Gln Ala Asp Phe Thr Ser Leu Pro His Leu 485 490 495	1785
ttg tat caa caa ttg ggg cat tat cgt agt cag gaa gca gtc aca Leu Tyr Gln Gln Leu Gly His Tyr Arg Ser Gln Glu Ala Ala Val Thr 500 505 510	1833

<210> 71
<211> 536
<212> PRT
<213> Pasteurella multocida

<400> 71
Met Phe Lys Arg Phe Arg Ala Phe Thr Tyr Arg Pro Ala Ser Tyr Leu
1 5 10 15
Gly Gly Met Leu Val Ile Val Phe Leu Ser Ala Phe Tyr Ala Phe Ala
20 25 30
Leu Gly Ala Val Phe Ser Leu Pro Phe Ala Arg Ser Trp Thr Ala Leu
35 40 45
Leu Ser Asp Gln Tyr Leu Gln His Val Ile Ile Phe Ser Phe Trp Gln
50 55 60
Ala Phe Leu Ser Ala Val Leu Ala Val Leu Phe Gly Gly Ile Val Ala
65 70 75 80
Arg Ala Phe Phe Tyr Gln Pro Phe Val Gly Lys Lys Leu Ile Leu Lys
85 90 95
Leu Phe Ser Leu Thr Phe Val Leu Pro Ala Leu Val Ala Ile Phe Gly
100 105 110
Leu Leu Gly Val Tyr Gly Ala Ser Gly Trp Leu Ala Met Leu Ser Gln
115 120 125
Phe Phe Ala Trp Asp Trp Thr Pro Asn Ile Tyr Gly Leu Thr Gly Ile
130 135 140
Leu Leu Ala His Leu Phe Phe Asn Val Pro Leu Ala Cys Arg Leu Phe
145 150 155 160
Leu Gln Gly Leu Gln Ala Ile Pro Val Gln Gln Arg Gln Leu Ala Ala
165 170 175
Gln Leu Asn Leu Arg Gly Trp His Phe Ile Arg Leu Ile Glu Trp Pro
180 185 190
Tyr Leu Arg Gln Gln Leu Leu Pro Ala Phe Thr Leu Ile Phe Met Leu
195 200 205
Cys Phe Thr Ser Phe Ala Ile Val Leu Thr Leu Gly Gly Pro Lys
210 215 220
Tyr Thr Thr Leu Glu Val Ala Ile Tyr Gln Ala Ile Leu Phe Glu Phe
225 230 235 240
Asp Val Pro Lys Ala Gly Leu Phe Ala Leu Leu Gln Phe Val Phe Cys
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Phe Leu Leu Phe Thr Leu Ser Ser Phe Phe Ser Pro Ala Pro Ala Thr
260 265 270
Thr Leu His Ser Gln Pro Thr Trp Phe Ala Pro Gln Ser Tyr Trp Val
275 280 285
Lys Leu Trp Gln Arg Met Ile Ile Val Cys Ala Thr Val Phe Ile Leu
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Leu Pro Leu Leu Asn Thr Leu Val Ser Ala Leu Leu Ser Ser Gln Phe
 305 310 315 320
 Phe Thr Leu Trp Leu Gln Pro Gln Leu Trp Lys Ala Leu Gly Tyr Ser
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 Leu Thr Ile Ala Pro Thr Ser Ala Leu Leu Ala Leu Val Leu Ser Phe
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 Ala Leu Leu Leu Leu Ala Arg Glu Leu His Trp Arg His Tyr Arg Ser
 355 360 365
 Leu Ser His Val Ile Leu Asn Ile Gly Ala Thr Ile Leu Ala Ile Pro
 370 375 380
 Thr Leu Val Leu Ala Ile Gly Leu Phe Ile Leu Leu Arg Glu Ile Asp
 385 390 395 400
 Phe Ser Pro Tyr His Leu Phe Gly Val Val Val Cys Cys Asn Ala Leu
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 Ala Ala Met Pro Phe Val Leu Arg Ile Leu Ala Leu Pro Met His Asn
 420 425 430
 Asn Met Ile Tyr Tyr Glu Lys Leu Cys Gln Ser Leu Asn Leu Arg Gly
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 Trp Gln Arg Phe Arg Leu Ile Glu Trp His Lys Leu Arg Ala Pro Met
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 Lys Tyr Ala Phe Ala Leu Ala Cys Ala Leu Ser Leu Gly Asp Phe Thr
 465 470 475 480
 Ala Ile Ala Leu Phe Gly Gln Ala Asp Phe Thr Ser Leu Pro His Leu
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 Leu Tyr Gln Gln Leu Gly His Tyr Arg Ser Gln Glu Ala Ala Val Thr
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acatgccatt tccagcaatt gaaaaaagtt tcttctttat ttc atg cct cat cat 1555
Met Pro His His

tgt tgt tct ttc agt act aca tat att ccg tca cat cta tac aaa ata	1603
Cys Cys Ser Phe Ser Thr Thr Tyr Ile Pro Ser His Leu Tyr Lys Ile	
5 10 15 20	
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Ser Gly Gly Ile Ile Met Ile Ser Ala Phe Gly Ile Gly Ile Gly Thr	
25 30 35	

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cta aaa cat aca atc aat act gtt ggt atg ata atc tgg gtc ggc att Leu Lys His Thr Ile Asn Thr Val Gly Met Ile Ile Trp Val Gly Ile 310 315 320	2515
ggc gca aca atg att ata ggt att tat aat cta atg ggt ggg gac cga Gly Ala Thr Met Ile Ile Gly Ile Tyr Asn Leu Met Gly Gly Asp Arg 325 330 335 340	2563
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atc att att atg atg gtt att tta tta ata ctt ggt atg ttc tta gat Ile Ile Ile Met Met Val Ile Leu Ile Leu Gly Met Phe Leu Asp 360 365 370	2659
tgg att ggt gtt gcc atg ttg act ttc ctc aag aca agt aaa gcg aca Trp Ile Gly Val Ala Met Leu Thr Phe Leu Lys Thr Ser Lys Ala Thr 375 380 385	2707
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tcc ttc cac agt acc aat gtt cat cgt ggt acc ttt gtc ggg cgc ggt Ser Phe His Ser Thr Asn Val His Arg Gly Thr Phe Val Gly Arg Gly 405 410 415 420	2803
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Ile Gly Met Pro Leu Gly Phe Leu Thr Gly Leu Ile Ala Leu Val Ile
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 Ser Tyr Leu Trp Phe Asp Thr Thr Ala Ile Met Gln Met Ile Ala Ser
 65 70 75 80
 Arg Val Thr Asp Phe Thr Ser Ser Tyr Thr Phe Val Ala Val Pro Met
 85 90 95
 Phe Val Leu Met Ala Thr Leu Leu Asp Lys Thr Gly Ile Ala Arg Asp
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 Leu Tyr Asn Ala Met Arg Val Ile Gly Gly Arg Leu Arg Gly Gly Ile
 115 120 125
 Ala Ile Gln Ser Met Phe Val Ala Val Leu Leu Ala Thr Met Ser Gly
 130 135 140
 Ile Ile Gly Gly Glu Thr Val Leu Leu Gly Met Leu Ala Leu Pro Gln
 145 150 155 160
 Met Leu Arg Leu Gly Tyr Asn Lys Asn Leu Ala Ile Gly Thr Val Val
 165 170 175
 Ala Gly Gly Ala Leu Gly Thr Met Val Pro Pro Ser Ile Val Leu Ile
 180 185 190
 Ile Tyr Gly Met Thr Ala Asn Val Ser Ile Gly Glu Leu Phe Leu Ala
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 Ala Ile Pro Ala Ser Leu Leu Ser Thr Phe Tyr Ile Leu Tyr Ile
 210 215 220
 Leu Val Leu Cys Tyr Phe Lys Pro Ser Tyr Gly Pro Ala Met Pro Ser
 225 230 235 240
 Ser Glu Asn His Thr Leu Thr Lys Glu Asp Ile Lys Lys Ile Ile His
 245 250 255
 Asp Ile Ala Ile Pro Val Ala Ile Ala Thr Trp Ile Leu Gly Ser Ile
 260 265 270
 Tyr Gly Gly Ile Ala Ser Ile Thr Glu Ser Ala Cys Val Gly Val Val
 275 280 285
 Gly Val Ile Leu Ala Ala Phe Tyr Arg Lys Glu Leu Asn Phe Lys Ile
 290 295 300
 Val Gln Glu Ser Leu Lys His Thr Ile Asn Thr Val Gly Met Ile Ile
 305 310 315 320
 Trp Val Gly Ile Gly Ala Thr Met Ile Ile Gly Ile Tyr Asn Leu Met
 325 330 335
 Gly Gly Asp Arg Phe Ile Ala Asn Leu Phe Ala Ser Leu Asp Ala Ser
 340 345 350
 Pro Ile Tyr Thr Ile Ile Ile Met Met Val Ile Leu Leu Ile Leu Gly
 355 360 365
 Met Phe Leu Asp Trp Ile Gly Val Ala Met Leu Thr Phe Leu Lys Thr
 370 375 380

Ser Lys Ala Thr Ile Asn Leu Cys Phe Asp Ile Val Arg Tyr Ser Ile
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Trp Arg Gly Pro Ser Phe His Ser Thr Asn Val His Arg Gly Thr Phe
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Val Gly Arg Gly Thr Phe
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 Met Val Leu Pro

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 Ile Ile Ser Thr Pro Lys Leu Trp Gln Tyr Ile Pro Ser Ser Lys Leu
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gaa caa tcc gcc atg gct aaa caa cct aat tct ttg att cgt tta ata 570
 Glu Gln Ser Ala Met Ala Lys Gln Pro Asn Ser Leu Ile Arg Leu Ile
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atg gct tca cgt gta gtt gga cgg acg cga tcg gta cca tca aaa gca 618
 Met Ala Ser Arg Val Val Gly Arg Thr Arg Ser Val Pro Ser Lys Ala
 40 45 50

ata ata tcg gcg cct gct gcg gct aac tct tca atg tct tgt aaa aat 666
 Ile Ile Ser Ala Pro Ala Ala Asn Ser Ser Met Ser Cys Lys Asn
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ggg cta ata cga acg gga ctg tca ggt aaa tcg cgt tta acg ata cca 714
 Gly Leu Ile Arg Thr Gly Leu Ser Gly Lys Ser Arg Leu Thr Ile Pro
 70 75 80

ata atc ggt aca ttg acg acg tta cgc gtg gct ttt aaa ttt tcg atc 762
 Ile Ile Gly Thr Leu Thr Leu Arg Val Ala Phe Lys Phe Ser Ile

| 85 | 90 | 95 | 100 | |
|---|-------------------------|----|-----|------|
| cct tca ata cgt aac ccg gca gca cca ccg | ata acg gat gct tgc gcc | | | 810 |
| Pro Ser Ile Arg Asn Pro Ala Ala Pro Pro | Ile Thr Asp Ala Cys Ala | | | |
| 105 | 110 | | 115 | |
| atg gcg gca aca att tct ggc gag tcc att ggc cca tta tct acg ggc | | | | 858 |
| Met Ala Ala Thr Ile Ser Gly Glu Ser Ile Gly Pro Leu Ser Thr Gly | | | | |
| 120 | 125 | | 130 | |
| tgg caa gat gcg att aag cca tat tta att tgt tct aaa act tgc gga | | | | 906 |
| Trp Gln Asp Ala Ile Lys Pro Tyr Leu Ile Cys Ser Lys Thr Cys Gly | | | | |
| 135 | 140 | | 145 | |
| tgt gat agt ttt gac ata tta act cca gtc taaaatttac aaaagaagat | | | | 956 |
| Cys Asp Ser Phe Asp Ile Leu Thr Pro Val | | | | |
| 150 | 155 | | | |
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| ttgtcaatcc ttgttatattt ttgtgtttgc tgggttgcga tacactgttc taatattgct | | | | 1136 |
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| caaatatcat tgacgcctaa aaaaagaaaa acagattgtc caagttgttgc aatccgttta | | | | 1496 |
| ggtttaacga taacatccaa atattgtcgc gtactgacgc cagaaagtcc taaaattggcg | | | | 1556 |
| acggtttgcg ccgctaattt aggtgtgcct gctacctgtt cgccccacat gtcaaaaagt | | | | 1616 |
| gaatgaccaa ttaagctgat attggcaggt ttggaaaatt ccgcattttt gctctgatag | | | | 1676 |
| cgttgataaa tattcctgatc acttagcatg tggaccttc tattttgaaa taaaacgcta | | | | 1736 |
| agtattataat aaaaacctgat atgcccgtaa acagtaaact tatctccgt agggtaaat | | | | 1796 |
| attcaattttt gtgacgaacc tattcattat gaaataaaac ttcattttct atataaaaaaa | | | | 1856 |
| tagtttttc actttagaat gccaacgtg tgaaattttt ttcatcatca tttaacgta | | | | 1916 |
| atcccaacgt aaccaataga ggagaactca taatgaaatt taaaaacta ctacttgcatt | | | | 1976 |
| ctttatgttt aggtgtttca gttctgtat ttgcagcaga ttacgatctt aaattcggtt | | | | 2036 |
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| aagaaaaatc caatggcaaa attgatgtgg tattttccc tagtcacag ttaggtgatg | | | | 2156 |
| accgtgtat gattaaacaa taaaagacg gtgcattaga ctttacgtta ggtgaatcag | | | | 2216 |
| cacgtttcca aatttacttc ccagaagcag aagtattgc gttgcctt atgattccta | | | | 2276 |
| attttgaaac ctctaaaaaa gcgttgctcg acacaaaatt tggtcaaggt ttattgaaaa | | | | 2336 |

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 35 40 45
 Pro Ser Lys Ala Ile Ile Ser Ala Pro Ala Ala Asn Ser Ser Met
 50 55 60
 Ser Cys Lys Asn Gly Leu Ile Arg Thr Gly Leu Ser Gly Lys Ser Arg
 65 70 75 80
 Leu Thr Ile Pro Ile Ile Gly Thr Leu Thr Thr Leu Arg Val Ala Phe
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 Lys Phe Ser Ile Pro Ser Ile Arg Asn Pro Ala Ala Pro Pro Ile Thr
 100 105 110
 Asp Ala Cys Ala Met Ala Ala Thr Ile Ser Gly Glu Ser Ile Gly Pro
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 caacgtaacc aatagaggag aactcata atg aaa ttt aaa aaa cta cta ctt 1972
 Met Lys Phe Lys Lys Leu Leu Leu
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gca gta gaa ttc ttt gcg aaa gaa gtg aaa gaa aaa tcc aat ggc aaa 2116
 Ala Val Glu Phe Phe Ala Lys Glu Val Lys Glu Lys Ser Asn Gly Lys
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 Ile Asp Val Ala Ile Phe Pro Ser Ser Gln Leu Gly Asp Asp Arg Val
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cct tat atg att cct aat ttt gaa acc tct aaa aaa gcg ttg ctc gac 2308
 Pro Tyr Met Ile Pro Asn Phe Glu Thr Ser Lys Lys Ala Leu Leu Asp
 105 110 115 120

aca aaa ttt ggt caa ggt tta ttg aaa aaa att gat aaa gag tta aac 2356
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 125 130 135

gta caa gtg tta tct gtg gcg tat aac ggt aca cgt caa aca act tct 2404
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 140 145 150

aac cgt gca atc aac agc att gaa gac atg aaa ggg tta aaa tta cgt 2452
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 155 160 165

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 Val Pro Asn Ala Ala Thr Asn Leu Ala Tyr Ala Lys Tyr Val Gly Ala
 170 175 180

gcg cca aca cca atg gca ttc tct gaa gtt tac ctt gcg ctt caa aca 2548
 Ala Pro Thr Pro Met Ala Phe Ser Glu Val Tyr Leu Ala Leu Gln Thr
 185 190 195 200

aac tct gtg gat ggt caa gaa aac cca tta ccg aca atc caa gca caa 2596
 Asn Ser Val Asp Gly Gln Glu Asn Pro Leu Pro Thr Ile Gln Ala Gln
 205 210 215

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 Lys Phe Tyr Glu Val Gln Lys Tyr Leu Ala Leu Thr Asn His Ile Leu
 220 225 230

| | |
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| Asn Asp Gln Leu Tyr Leu Ile Ser Asn Asp Thr Leu Ala Asp Leu Pro | |
| 235 | 240 |
| | 245 |
| gaa gat tta caa aaa gtg gtt aaa gat gca gca gcg aaa gcc gct gaa | 2740 |
| Glu Asp Leu Gln Lys Val Val Lys Asp Ala Ala Lys Ala Ala Glu | |
| 250 | 255 |
| | 260 |
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| | 10 |
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| Ala Ser Val Phe Ala Ala Asp Tyr Asp Leu Lys Phe Gly Met Val Ala | |
| 20 | 25 |
| | 30 |
| Gly Pro Ser Ser Asn Glu Tyr Lys Ala Val Glu Phe Phe Ala Lys Glu | |
| 35 | 40 |
| | 45 |
| Val Lys Glu Lys Ser Asn Gly Lys Ile Asp Val Ala Ile Phe Pro Ser | |
| 50 | 55 |
| | 60 |
| Ser Gln Leu Gly Asp Asp Arg Val Met Ile Lys Gln Leu Lys Asp Gly | |
| 65 | 70 |
| | 75 |
| | 80 |
| Ala Leu Asp Phe Thr Leu Gly Glu Ser Ala Arg Phe Gln Ile Tyr Phe | |
| 85 | 90 |
| | 95 |
| Pro Glu Ala Glu Val Phe Ala Leu Pro Tyr Met Ile Pro Asn Phe Glu | |
| 100 | 105 |
| | 110 |
| Thr Ser Lys Lys Ala Leu Leu Asp Thr Lys Phe Gly Gln Gly Leu Leu | |
| 115 | 120 |
| | 125 |
| Lys Lys Ile Asp Lys Glu Leu Asn Val Gln Val Leu Ser Val Ala Tyr | |
| 130 | 135 |
| | 140 |
| Asn Gly Thr Arg Gln Thr Thr Ser Asn Arg Ala Ile Asn Ser Ile Glu | |
| 145 | 150 |
| | 155 |
| | 160 |
| Asp Met Lys Gly Leu Lys Leu Arg Val Pro Asn Ala Ala Thr Asn Leu | |
| 165 | 170 |
| | 175 |
| Ala Tyr Ala Lys Tyr Val Gly Ala Ala Pro Thr Pro Met Ala Phe Ser | |
| 180 | 185 |
| | 190 |
| Glu Val Tyr Leu Ala Leu Gln Thr Asn Ser Val Asp Gly Gln Glu Asn | |
| 195 | 200 |
| | 205 |
| Pro Leu Pro Thr Ile Gln Ala Gln Lys Phe Tyr Glu Val Gln Lys Tyr | |
| 210 | 215 |
| | 220 |
| Leu Ala Leu Thr Asn His Ile Leu Asn Asp Gln Leu Tyr Leu Ile Ser | |
| 225 | 230 |
| | 235 |
| | 240 |

Asn Asp Thr Leu Ala Asp Leu Pro Glu Asp Leu Gln Lys Val Val Lys
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Asp Ala Ala Ala Lys Ala Ala Glu Tyr His Thr Lys Leu Phe Val Asp
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Gly Glu Asn Ser Leu Val Glu
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 Met Thr Lys Val Ile His Thr Asp Asn Ala Pro Ala Ala Ile

1

5

10

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 Gly Pro Tyr Val Gln Ala Val Asp Leu Gly Asn Met Leu Leu Thr Ser
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35

40

45

| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|---|------|-----|-----|---|------|---|------|--|------|--|------|--|------|--|------|--|------|--|------|--|------|--|------|--|------|--|------|--|------|--|------|--|------|--|------|--|------|---|------|---|------|--|------|--|------|--|------|---|------|---|------|--|------|--|------|--|------|---|------|---|------|---|------|--|------|---|------|---|------|---|------|--|------|---|------|---|------|---|------|---|------|
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| Val Ala Gln Ala Arg Gln Ser Leu Glu Asn Val Lys Ala Ile Val Glu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 50 | 55 | 55 | 60 | caa gcg gga tta caa gtc gca aat atc gtg aaa acc acg gtg ttt gtg | 1141 | Gln Ala Gly Leu Gln Val Ala Asn Ile Val Lys Thr Thr Val Phe Val | | 65 | 70 | 70 | 75 | aaa gat tta aat gac ttt gca g.g gtc aat gcg gag tat gaa cgt ttc | 1189 | Lys Asp Leu Asn Asp Phe Ala Ala Val Asn Ala Glu Tyr Glu Arg Phe | | 80 | 85 | 85 | 90 | ttt aaa gag aac aat cac cct agc ttc cct gct cgt tca tgt gtg gaa | 1237 | Phe Lys Glu Asn Asn His Pro Ser Phe Pro Ala Arg Ser Cys Val Glu | | 95 | 100 | 100 | 105 | 105 | 110 | gtg gca cgt ttg ccg aaa gat gtg ggg att gaa atc gag gca atc gct | 1285 | Val Ala Arg Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala | | 115 | 120 | 120 | 125 | 125 | | gta aaa gcc taatgaatacg cttgcattta tcttagtcgt agcaaaaacaa | 1334 | Val Lys Ala | | tctctttca cttgctctct ccaaagcaag ttgataagtg atttttattt ggcgtttttc | 1394 | tattgatacg caaaaaacgcc cttaactgat agagaataaa ctatgcaaaa tcaagtcatc | 1454 | gagattctac aataccgttt aaaaccacaa tcaggacaaa cgtttccacca aattatgcgt | 1514 | gagatcagtg ttccactcca taaacaacat gggattgatg tcattgcgtt tgaaattca | 1574 | ttacatgata ttgacagcta ttatattaatc cgtgcatttg agacagaaac caaattgcaa | 1634 | cagcagctcg atgctttta tgccagtgtat gattggcgtg atggaccaag agaaaagtatc | 1694 | attcgccctga ttgaaaggcag tttaaaatcg gtgatcatgc tcccacaca ggcaatccat | 1754 | gcactacgca accattatcc tcaataaaaat caacaaccgc acccaatcag tgcgttcatt | 1814 | ttttcttact ttttcagtgc taagggaaaa acaacgtatg tggacgttgt ttaatcaatt | 1874 | tccaaacaca ttgcgcgata tcacaccaac tctcaatttc tgtttctaaa gaacgcagcg | 1934 | caaccataaa cgcgataaaag aaactgacaa tcaaattcac cataccaatc aataacacga | 1994 | acactaaacc ttgttataaac acatgccaag taaacgcgc actgatcgcc atatagcccc | 2054 | aattcgcaga agaaaacgcc acatggcga tatctaacgg taaattaagc aaatacccgaa | 2114 | ctaaccctgt taaaccaagc aataaaccac aacacagatt tcccataatc gaaccgtaat | 2174 | tatcatgcca gtattctgca aattttgtatc gcatattacg ggtcaacaga cggcgtaaaa | 2234 | tagggtgatt tcttagtcgc attttttaagt tcaaataatt actacgatata tcaaataaac | 2294 | cagaaataat cccagaaaag aataaccaga aacccgcaat ggccggaaac cataaggacc | 2354 | ctttcatcggt atcaaggat ttttgggtt aggcaatctc cgcgtcactc aataaagggtg | 2414 | taccaacata atgttatacg ccttagcgca gcaaacaagc cacagaaatc gctaaagtga | 2474 |
| 55 | 60 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| caa gcg gga tta caa gtc gca aat atc gtg aaa acc acg gtg ttt gtg | 1141 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Gln Ala Gly Leu Gln Val Ala Asn Ile Val Lys Thr Thr Val Phe Val | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| 70 | 75 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| aaa gat tta aat gac ttt gca g.g gtc aat gcg gag tat gaa cgt ttc | 1189 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Lys Asp Leu Asn Asp Phe Ala Ala Val Asn Ala Glu Tyr Glu Arg Phe | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 80 | 85 | 85 | 90 | ttt aaa gag aac aat cac cct agc ttc cct gct cgt tca tgt gtg gaa | 1237 | Phe Lys Glu Asn Asn His Pro Ser Phe Pro Ala Arg Ser Cys Val Glu | | 95 | 100 | 100 | 105 | 105 | 110 | gtg gca cgt ttg ccg aaa gat gtg ggg att gaa atc gag gca atc gct | 1285 | Val Ala Arg Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala | | 115 | 120 | 120 | 125 | 125 | | gta aaa gcc taatgaatacg cttgcattta tcttagtcgt agcaaaaacaa | 1334 | Val Lys Ala | | tctctttca cttgctctct ccaaagcaag ttgataagtg atttttattt ggcgtttttc | 1394 | tattgatacg caaaaaacgcc cttaactgat agagaataaa ctatgcaaaa tcaagtcatc | 1454 | gagattctac aataccgttt aaaaccacaa tcaggacaaa cgtttccacca aattatgcgt | 1514 | gagatcagtg ttccactcca taaacaacat gggattgatg tcattgcgtt tgaaattca | 1574 | ttacatgata ttgacagcta ttatattaatc cgtgcatttg agacagaaac caaattgcaa | 1634 | cagcagctcg atgctttta tgccagtgtat gattggcgtg atggaccaag agaaaagtatc | 1694 | attcgccctga ttgaaaggcag tttaaaatcg gtgatcatgc tcccacaca ggcaatccat | 1754 | gcactacgca accattatcc tcaataaaaat caacaaccgc acccaatcag tgcgttcatt | 1814 | ttttcttact ttttcagtgc taagggaaaa acaacgtatg tggacgttgt ttaatcaatt | 1874 | tccaaacaca ttgcgcgata tcacaccaac tctcaatttc tgtttctaaa gaacgcagcg | 1934 | caaccataaa cgcgataaaag aaactgacaa tcaaattcac cataccaatc aataacacga | 1994 | acactaaacc ttgttataaac acatgccaag taaacgcgc actgatcgcc atatagcccc | 2054 | aattcgcaga agaaaacgcc acatggcga tatctaacgg taaattaagc aaatacccgaa | 2114 | ctaaccctgt taaaccaagc aataaaccac aacacagatt tcccataatc gaaccgtaat | 2174 | tatcatgcca gtattctgca aattttgtatc gcatattacg ggtcaacaga cggcgtaaaa | 2234 | tagggtgatt tcttagtcgc attttttaagt tcaaataatt actacgatata tcaaataaac | 2294 | cagaaataat cccagaaaag aataaccaga aacccgcaat ggccggaaac cataaggacc | 2354 | ctttcatcggt atcaaggat ttttgggtt aggcaatctc cgcgtcactc aataaagggtg | 2414 | taccaacata atgttatacg ccttagcgca gcaaacaagc cacagaaatc gctaaagtga | 2474 | | | | | | | | | | | | | | | | |
| 85 | 90 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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| Phe Lys Glu Asn Asn His Pro Ser Phe Pro Ala Arg Ser Cys Val Glu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 95 | 100 | 100 | 105 | 105 | 110 | gtg gca cgt ttg ccg aaa gat gtg ggg att gaa atc gag gca atc gct | 1285 | Val Ala Arg Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala | | 115 | 120 | 120 | 125 | 125 | | gta aaa gcc taatgaatacg cttgcattta tcttagtcgt agcaaaaacaa | 1334 | Val Lys Ala | | tctctttca cttgctctct ccaaagcaag ttgataagtg atttttattt ggcgtttttc | 1394 | tattgatacg caaaaaacgcc cttaactgat agagaataaa ctatgcaaaa tcaagtcatc | 1454 | gagattctac aataccgttt aaaaccacaa tcaggacaaa cgtttccacca aattatgcgt | 1514 | gagatcagtg ttccactcca taaacaacat gggattgatg tcattgcgtt tgaaattca | 1574 | ttacatgata ttgacagcta ttatattaatc cgtgcatttg agacagaaac caaattgcaa | 1634 | cagcagctcg atgctttta tgccagtgtat gattggcgtg atggaccaag agaaaagtatc | 1694 | attcgccctga ttgaaaggcag tttaaaatcg gtgatcatgc tcccacaca ggcaatccat | 1754 | gcactacgca accattatcc tcaataaaaat caacaaccgc acccaatcag tgcgttcatt | 1814 | ttttcttact ttttcagtgc taagggaaaa acaacgtatg tggacgttgt ttaatcaatt | 1874 | tccaaacaca ttgcgcgata tcacaccaac tctcaatttc tgtttctaaa gaacgcagcg | 1934 | caaccataaa cgcgataaaag aaactgacaa tcaaattcac cataccaatc aataacacga | 1994 | acactaaacc ttgttataaac acatgccaag taaacgcgc actgatcgcc atatagcccc | 2054 | aattcgcaga agaaaacgcc acatggcga tatctaacgg taaattaagc aaatacccgaa | 2114 | ctaaccctgt taaaccaagc aataaaccac aacacagatt tcccataatc gaaccgtaat | 2174 | tatcatgcca gtattctgca aattttgtatc gcatattacg ggtcaacaga cggcgtaaaa | 2234 | tagggtgatt tcttagtcgc attttttaagt tcaaataatt actacgatata tcaaataaac | 2294 | cagaaataat cccagaaaag aataaccaga aacccgcaat ggccggaaac cataaggacc | 2354 | ctttcatcggt atcaaggat ttttgggtt aggcaatctc cgcgtcactc aataaagggtg | 2414 | taccaacata atgttatacg ccttagcgca gcaaacaagc cacagaaatc gctaaagtga | 2474 | | | | | | | | | | | | | | | | | | | | | | | | |
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| Glu Thr Asn Arg Ile Val Asn Phe Val Gly Thr Pro Asp Met Ile Gly | | | |
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| Lys Phe Val Asp Ile Lys Ile Thr Asp Val Phe Thr Asn Ser Leu Arg | | | |
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| Gly Glu Val Val Arg Thr Glu Glu Gln Met Gly Leu Arg Val Val Gln | | | |
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| 1 | | | | 5 | | | | | 10 | | | | 15 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Asp | Ser | Ser | Lys | Met | Ala | Asp | Leu | Leu | Asn | Ser | Thr | His | Gly | Leu |
| | | | | | 20 | | | 25 | | | | 30 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Leu | Thr | Glu | Ile | Pro | Glu | Glu | Ala | Asp | Val | Leu | Leu | Leu | Asn | Thr |
| | | | | | 35 | | | 40 | | | | 45 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Ser | Ile | Arg | Glu | Lys | Ala | Gln | Glu | Lys | Val | Phe | His | Gln | Leu | Gly |
| | | | | | 50 | | | 55 | | | 60 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Trp | Lys | Glu | Leu | Lys | Lys | His | Lys | Pro | Gly | Leu | Val | Ile | Gly | Val |
| 65 | | | | | 70 | | | | 75 | | | 80 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Gly | Cys | Val | Ala | Ser | Gln | Glu | Gly | Glu | His | Ile | Arg | Thr | Arg | Ala |
| | | | | | 85 | | | 90 | | | 95 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Tyr | Val | Asp | Ile | Ile | Phe | Gly | Pro | Gln | Thr | Leu | His | Arg | Leu | Pro |
| | | | | | 100 | | | 105 | | | 110 | | | | |

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| Glu | Met | Ile | Asn | Gln | Ile | Arg | Gly | Gly | Lys | Ser | Ser | Val | Val | Asp | Val |
| | | | | | 115 | | | 120 | | | 125 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Phe | Pro | Glu | Ile | Glu | Lys | Phe | Asp | Arg | Leu | Pro | Glu | Pro | Arg | Ala |
| | | | | | 130 | | | 135 | | | 140 | | | | |

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 Glu Leu Val Ser Phe Leu His Leu Pro Val Gln Ser Gly Ser Asp Arg
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 Met Lys Lys
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| aca | gtt | gtg | aat | cct | gaa | cgt | cgt | cga | ttt | ttt | aaa | gag | gct | acg | cgc | 463 |
| Thr | Val | Val | Asn | Pro | Glu | Arg | Arg | Arg | Phe | Phe | Lys | Glu | Ala | Thr | Arg | |
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| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| act | gca | ggc | ggg | ttg | gca | ggg | gtg | act | ttg | ctc | ctt | ggt | ttg | caa | caa | 511 |
| Thr | Ala | Gly | Gly | Leu | Ala | Gly | Val | Thr | Leu | Leu | Leu | Gly | Leu | Gln | Gln | |
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| | | | | | | | | | | | | | | | | |
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| aag | cag | agt | ctt | gct | cgc | gaa | ggc | gtg | gct | tta | cgc | cca | cct | ttt | gcc | 559 |
| Lys | Gln | Ser | Leu | Ala | Arg | Glu | Gly | Val | Ala | Leu | Arg | Pro | Pro | Phe | Ala | |
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| | | | | | | | | | | | | | | | | |
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| ctt | gag | aat | gag | aaa | gct | ttt | tct | gct | gct | tgc | att | cgt | tgt | ggt | cag | 607 |
| Leu | Glu | Asn | Glu | Lys | Ala | Phe | Ser | Ala | Ala | Cys | Ile | Arg | Cys | Gly | Gln | |
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| | | | | | | | | | | | | | | | 60 | |
| | | | | | | | | | | | | | | | 65 | |

| | | | | | | | | | | | | | | | | |
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| tgt | gta | caa | gcc | tgt | cca | cat | gag | atg | ttg | cat | ctt | gcc | tca | ctg | att | 655 |
| Cys | Val | Gln | Ala | Cys | Pro | His | Glu | Met | Leu | His | Leu | Ala | Ser | Leu | Ile | |
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| | | | | | | | | | | | | | | | 75 | |
| | | | | | | | | | | | | | | | 80 | |

| | | | | | | | | | | | | | | | | |
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| tca | ccg | atg | gaa | gca | ggt | aca | ccg | tat | ttc | att | gct | cgc | gat | aag | ccc | 703 |
| Ser | Pro | Met | Glu | Ala | Gly | Thr | Pro | Tyr | Phe | Ile | Ala | Arg | Asp | Lys | Pro | |
| | | | | | | | | | | | | | | | 85 | |
| | | | | | | | | | | | | | | | 90 | |
| | | | | | | | | | | | | | | | 95 | |

| | | | | | | | | | | | | | | | | |
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| tgt | gaa | atg | tgt | gtg | gat | att | cct | tgt | gca | aaa | gcc | tgc | cca | acc | ggt | 751 |
| Cys | Glu | Met | Cys | Val | Asp | Ile | Pro | Cys | Ala | Lys | Ala | Cys | Pro | Thr | Gly | |
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| | | | | | | | | | | | | | | | | |
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| Ala | Leu | Asp | Asn | Gln | Ala | Thr | Glu | Ile | Asp | Asp | Ala | Arg | Met | Gly | Leu | |
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Cys Glu Glu Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro
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| agt | tca | agt | tta | ggt | ttc | tta | ata | ttg | aaa | act | gta | cca | tct | ttt | tca | 2689 |
| Ser | Ser | Ser | Leu | Gly | Phe | Leu | Ile | Leu | Lys | Thr | Val | Pro | Ser | Phe | Ser | |
| 80 | | | | | | | | | | | | | 90 | | | |
| tac | gtt | aca | atc | tca | aca | ctt | aat | cgc | gtt | tgaccccg | atttttgata | | | | | 2739 |
| Tyr | Val | Thr | Ile | Ser | Thr | Leu | Asn | Arg | Val | | | | | | | |
| 95 | | | | | | | | | | | | | 100 | | | |
| gtcaaagact | actgagtaac | gctttagtc | gcgtgaatcg | actgttacat | aagccgat | at | 2799 | | | | | | | | | |
| gtcagaataa | gtactgccgg | tatatacgct | taatctaaga | ttaagcttgc | cactttgtt | | 2859 | | | | | | | | | |
| cgataaagcg | tcaaacgaaa | gcacgacttt | accgtccttgc | acttccacct | gatcttcaat | | 2919 | | | | | | | | | |
| gagcaattga | cttagtgcg | ccaatcgacc | gttggcagtc | agtgtcgaa | tgccgtgatc | | 2979 | | | | | | | | | |
| cgtatcaage | tttacaccgc | tat | tttcc | ccagtttta | ttgagcttt | cactatgtt | 3039 | | | | | | | | | |
| cagtaagttt | ctgccaccaa | tctgcaactg | attaaactta | gcttcaagcg | tttcaactt | | 3099 | | | | | | | | | |
| gactgcaagc | gacttgtttt | cattgtaac | cgtctgctca | agtgtgtga | ttttggatgt | | 3159 | | | | | | | | | |
| taaatctaac | ttagttgcat | tgacttcatc | agtccattct | gactttaact | ctttctcgc | | 3219 | | | | | | | | | |
| aagtgacgcc | acttcatctt | tgctagctt | cgtttttttt | aagtcagaaa | tgccactagt | | 3279 | | | | | | | | | |
| at | tttgcgc | actttagaat | cgagcgttc | tagtttgt | gagaaagatt | tgtctttt | 3339 | | | | | | | | | |
| gctagccgtt | tttgaatta | gctgtatttgc | actttcgctc | aatccaactc | tagcagttag | | 3399 | | | | | | | | | |
| actgtctagc | ttgtcagcag | tagatttatt | cacagtcgt | tgtgattgct | tgtgttgaat | | 3459 | | | | | | | | | |
| aatatccgcg | tttacttccg | agatagccac | gtcga | | | | 3494 | | | | | | | | | |
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| <211> | 103 | | | | | | | | | | | | | | | |
| <212> | PRT | | | | | | | | | | | | | | | |
| <213> | Pasteurella multocida | | | | | | | | | | | | | | | |
| <400> | 85 | | | | | | | | | | | | | | | |
| Met | Thr | Lys | Leu | Ser | Ile | Gln | Arg | Asp | Asn | Leu | Ile | Cys | Leu | Ser | Tyr | |
| 1 | | | | | | | | | | | | | | | 15 | |
| Val | Ala | Leu | Met | Gly | Phe | Gly | Phe | Pro | Ile | Met | Arg | Tyr | Met | Ser | Ile | |
| | | | | | | | | | | | | | | | | |
| 20 | | | | | | | | | | | | | | | 30 | |
| His | Phe | Asp | Thr | Leu | Asn | Asn | Ala | Val | Arg | Phe | Leu | Ser | Gly | Gly | | |
| | | | | | | | | | | | | | | | | |
| 35 | | | | | | | | | | | | | | 45 | | |
| Ser | Val | Phe | Ile | Leu | Ala | Cys | Phe | Phe | Tyr | Tyr | Arg | Ala | Glu | Leu | Thr | |
| | | | | | | | | | | | | | | | | |
| 50 | | | | | | | | | | | | | | 60 | | |
| Ser | Ser | Gly | Ala | Gly | Val | Gln | Ser | Val | Ala | Met | Leu | Pro | Ser | Ser | Ser | |
| | | | | | | | | | | | | | | | | |
| 65 | | | | | | | | | | | | | | 80 | | |
| Leu | Gly | Phe | Leu | Ile | Leu | Lys | Thr | Val | Pro | Ser | Phe | Ser | Tyr | Val | Thr | |
| | | | | | | | | | | | | | | | | |
| 85 | | | | | | | | | | | | | | 95 | | |
| Ile | Ser | Thr | Leu | Asn | Arg | Val | | | | | | | | | | |

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<210> 86
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 86
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19

<210> 87
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<220>
<223> Description of Artificial Sequence: PRIMER

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cggccggta cggcctagg

19

<210> 88
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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catggtaccc attctaac

18

<210> 89
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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18

<210> 90
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insert

<220>

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<223> N = A or T or G or C

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<211> 18
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<220>
<223> Description of Artificial Sequence: primer
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<400> 91
tacctacaac ctcaagct 18

<210> 92
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<220>
<223> Description of Artificial Sequence: primer

<400> 92
taccatttct aaccaagc 18

<210> 93
<211> 19
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 93
tacctacaac ctcaagctt 19

<210> 94
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<220>
<223> Description of Artificial Sequence: primer

<400> 94
taccatttct aaccaagctt 20

<210> 95
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 95
ggcagagcat tacgctgac 19

<210> 96
<211> 27
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

<400> 96
gtaccggcca ggcggccacg cgtattc 27

<210> 97
<211> 531
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<213> *Actinobacillus pleuropneumoniae*

<220>
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<400> 97
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atgttatgaa atgatatacg cgtccgaaa cggagaagtg gatcggttt acgtcgctt 180
caaccgtttt gaaaatacga tgcacaaaa acctgttac gcacagttac ttccgttacc 240
taaactatgat gacgatgaat tagatacgaa aggttcatgg gattatattt atgaaccgaa 300
tccacaagtt ttattggata gtttacttgt tcgttattta gaaactcagg tataccaagc 360
agttgtatgat aaccttagctt ctgaaacaagc cgctcgatg gtacgtatg aagccgcaac 420
agataatgctt ggtacattaa tcgatgaatt acaatttagtg tataacaaag ctcgccaagc 480
aagcattaca aatgaattaa acgaaattgt tgccgtgcc gcagcaattt a 531

<210> 98
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer
<400> 98
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<210> 99
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer
<400> 99
ggattacagc cggatccggg 20

<210> 100
<211> 1034
<212> DNA
<213> *Pasteurella multocida*

<220>
<223> cap5E

<220>
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<222> (1)..(1032)

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| atg ttt aaa aat aaa aca ctt tta att aca ggt gga acg ggt tct ttt | | | | 48 |
| Met Phe Lys Asn Lys Thr Leu Leu Ile Thr Gly Gly Thr Gly Ser Phe | | | | |
| 1 | 5 | 10 | 15 | |
| ggt aat gct gta ctc aaa cgt ttc tta gaa aca gat att cga gaa att | | | | 96 |
| Gly Asn Ala Val Leu Lys Arg Phe Leu Glu Thr Asp Ile Arg Glu Ile | | | | |
| 20 | 25 | 30 | | |
| cgt gtt ttt tcg cgt gat gag aag aaa caa gat gac atg cgg aaa aaa | | | | 144 |
| Arg Val Phe Ser Arg Asp Glu Lys Lys Gln Asp Asp Met Arg Lys Lys | | | | |
| 35 | 40 | 45 | | |
| tat aat gat gca aaa tta aaa ttt tat att ggc gat gtt cgt gac tac | | | | 192 |
| Tyr Asn Asp Ala Lys Leu Lys Phe Tyr Ile Gly Asp Val Arg Asp Tyr | | | | |
| 50 | 55 | 60 | | |
| gat agt att tta aat gcc tcg cga ggt gtt gac tat att tat cat gct | | | | 240 |
| Asp Ser Ile Leu Asn Ala Ser Arg Gly Val Asp Tyr Ile Tyr His Ala | | | | |
| 65 | 70 | 75 | 80 | |
| gcc gca tta aag caa gtg cct tca tgc gag ttt tat ccg tta gag gca | | | | 288 |
| Ala Ala Leu Lys Gln Val Pro Ser Cys Glu Phe Tyr Pro Leu Glu Ala | | | | |
| 85 | 90 | 95 | | |
| gtg aaa acc aat att tta ggt acg gca aat gtc tta gaa gcc gcc atc | | | | 336 |
| Val Lys Thr Asn Ile Leu Gly Thr Ala Asn Val Leu Glu Ala Ala Ile | | | | |
| 100 | 105 | 110 | | |
| caa aac cag ata aaa cgc gtc gtc tgt ctt agc aca gat aaa gcg gtg | | | | 384 |
| Gln Asn Gln Ile Lys Arg Val Val Cys Leu Ser Thr Asp Lys Ala Val | | | | |
| 115 | 120 | 125 | | |
| tac cca att aat gcg atg ggc att tct aaa gca atg atg gaa aaa gtc | | | | 432 |
| Tyr Pro Ile Asn Ala Met Gly Ile Ser Lys Ala Met Met Glu Lys Val | | | | |
| 130 | 135 | 140 | | |
| atc atc gca aaa tcg cgt aac cta gaa ggc aca cca acg aca atc tgt | | | | 480 |
| Ile Ile Ala Lys Ser Arg Asn Leu Glu Gly Thr Pro Thr Thr Ile Cys | | | | |
| 145 | 150 | 155 | 160 | |
| tgt act cgc tat ggc aat gtc atg gca tcg cgt ggt tcg gtt atc cca | | | | 528 |
| Cys Thr Arg Tyr Gly Asn Val Met Ala Ser Arg Gly Ser Val Ile Pro | | | | |
| 165 | 170 | 175 | | |
| tta ttt gtc gat caa ata cgt caa ggc aag cct ttt act att act gat | | | | 576 |
| Leu Phe Val Asp Gln Ile Arg Gln Gly Lys Pro Phe Thr Ile Thr Asp | | | | |
| 180 | 185 | 190 | | |
| cct gag atg aca cgc ttt atg atg aca ttg gaa gat gct gtg gat tta | | | | 624 |
| Pro Glu Met Thr Arg Phe Met Met Thr Leu Glu Asp Ala Val Asp Leu | | | | |
| 195 | 200 | 205 | | |
| gtc cta tat gca ttt aaa aat ggt caa aat ggt gat gtt ttt gta caa | | | | 672 |
| Val Leu Tyr Ala Phe Lys Asn Gly Gln Asn Gly Asp Val Phe Val Gln | | | | |
| 210 | 215 | 220 | | |
| aaa gcc ccc gca gca acc att ggt acc ctt gcc aaa gca att acc gaa | | | | 720 |
| Lys Ala Pro Ala Ala Thr Ile Gly Thr Leu Ala Lys Ala Ile Thr Glu | | | | |
| 225 | 230 | 235 | 240 | |
| tta tta tct gtc cca aat cac cct att tcc att ata ggt acg cgt cat | | | | 768 |
| Leu Leu Ser Val Pro Asn His Pro Ile Ser Ile Ile Gly Thr Arg His | | | | |

| 245 | 250 | 255 | |
|---|-----|-----|-----|
| gga gag aaa gca ttc gaa gct tta agc cgt gaa gaa atg gtt cat 816 | | | |
| Gly Glu Lys Ala Phe Glu Ala Leu Leu Ser Arg Glu Glu Met Val His | | | |
| 260 | 265 | 270 | |
| gca att aat gaa ggt aat tat tat cgc atc cca gcc gat caa cgc agt 864 | | | |
| Ala Ile Asn Glu Gly Asn Tyr Tyr Arg Ile Pro Ala Asp Gln Arg Ser | | | |
| 275 | 280 | 285 | |
| tta aat tac agt aaa tat gtc gaa aaa ggg gaa cca aaa att acc gaa 912 | | | |
| Leu Asn Tyr Ser Lys Tyr Val Glu Lys Gly Glu Pro Lys Ile Thr Glu | | | |
| 290 | 295 | 300 | |
| gtc acc gac tac aac tca cat aat act gag cgt ttg act gtc aag gaa 960 | | | |
| Val Thr Asp Tyr Asn Ser His Asn Thr Glu Arg Leu Thr Val Lys Glu | | | |
| 305 | 310 | 315 | 320 |
| atg aag cag tta ctg ctt aaa ctt gaa ttc ata cag aaa atg att gag 1008 | | | |
| Met Lys Gln Leu Leu Lys Leu Glu Phe Ile Gln Lys Met Ile Glu | | | |
| 325 | 330 | 335 | |
| ggt gaa tac atc tca ccg gag gta ta 1034 | | | |
| Gly Glu Tyr Ile Ser Pro Glu Val | | | |
| 340 | | | |
| <210> 101 | | | |
| <211> 344 | | | |
| <212> PRT | | | |
| <213> Pasteurella multocida | | | |
| <400> 101 | | | |
| Met Phe Lys Asn Lys Thr Leu Leu Ile Thr Gly Gly Thr Gly Ser Phe | | | |
| 1 | 5 | 10 | 15 |
| Gly Asn Ala Val Leu Lys Arg Phe Leu Glu Thr Asp Ile Arg Glu Ile | | | |
| 20 | 25 | 30 | |
| Arg Val Phe Ser Arg Asp Glu Lys Lys Gln Asp Asp Met Arg Lys Lys | | | |
| 35 | 40 | 45 | |
| Tyr Asn Asp Ala Lys Leu Lys Phe Tyr Ile Gly Asp Val Arg Asp Tyr | | | |
| 50 | 55 | 60 | |
| Asp Ser Ile Leu Asn Ala Ser Arg Gly Val Asp Tyr Ile Tyr His Ala | | | |
| 65 | 70 | 75 | 80 |
| Ala Ala Leu Lys Gln Val Pro Ser Cys Glu Phe Tyr Pro Leu Glu Ala | | | |
| 85 | 90 | 95 | |
| Val Lys Thr Asn Ile Leu Gly Thr Ala Asn Val Leu Glu Ala Ala Ile | | | |
| 100 | 105 | 110 | |
| Gln Asn Gln Ile Lys Arg Val Val Cys Leu Ser Thr Asp Lys Ala Val | | | |
| 115 | 120 | 125 | |
| Tyr Pro Ile Asn Ala Met Gly Ile Ser Lys Ala Met Met Glu Lys Val | | | |
| 130 | 135 | 140 | |
| Ile Ile Ala Lys Ser Arg Asn Leu Glu Gly Thr Pro Thr Thr Ile Cys | | | |
| 145 | 150 | 155 | 160 |

Cys Thr Arg Tyr Gly Asn Val Met Ala Ser Arg Gly Ser Val Ile Pro
 165 170 175
 Leu Phe Val Asp Gln Ile Arg Gln Gly Lys Pro Phe Thr Ile Thr Asp
 180 185 190
 Pro Glu Met Thr Arg Phe Met Met Thr Leu Glu Asp Ala Val Asp Leu
 195 200 205
 Val Leu Tyr Ala Phe Lys Asn Gly Gln Asn Gly Asp Val Phe Val Gln
 210 215 220
 Lys Ala Pro Ala Ala Thr Ile Gly Thr Leu Ala Lys Ala Ile Thr Glu
 225 230 235 240
 Leu Leu Ser Val Pro Asn His Pro Ile Ser Ile Ile Gly Thr Arg His
 245 250 255
 Gly Glu Lys Ala Phe Glu Ala Leu Leu Ser Arg Glu Glu Met Val His
 260 265 270
 Ala Ile Asn Glu Gly Asn Tyr Tyr Arg Ile Pro Ala Asp Gln Arg Ser
 275 280 285
 Leu Asn Tyr Ser Lys Tyr Val Glu Lys Gly Glu Pro Lys Ile Thr Glu
 290 295 300
 Val Thr Asp Tyr Asn Ser His Asn Thr Glu Arg Leu Thr Val Lys Glu
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 325 330 335
 Gly Glu Tyr Ile Ser Pro Glu Val
 340

<210> 102
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<220>
 <223> fhaB2

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 <222> (1) .. (4929)

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 1 5 10 15

ctc gtt cct gtg gca gaa tgt att aac tca gct att agc aat ggt tca 96
 Leu Val Pro Val Ala Glu Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser

| 20 | 25 | 30 | |
|--|------------|------------|-----|
| tct gat tca aca tcc aca tca gaa caa gtt gaa gag gaa cct ttc ctt
Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Glu Pro Phe Leu | 35
40 | 45 | 144 |
| cta gaa caa tat tca ctt tcc tcc gtg tct tta tta gta aaa agc acg
Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr | 50
55 | 60 | 192 |
| ttc aat cct gtt tcg tat gca atg caa ttg act tgg aaa cag ctt tct
Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser | 65
70 | 75
80 | 240 |
| att tta ttt tta act gtg att tct gtt cct gtt ttg gct gag gga aaa
Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys | 85
90 | 95 | 288 |
| ggg gat gaa aga aat caa tta aca gtg att gat aat agc gat cat att
Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile | 100
105 | 110 | 336 |
| aaa tta gat gca tct aat ctt gct ggt aat gat aaa aca aaa atc tat
Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr | 115
120 | 125 | 384 |
| caa gca gaa aat aaa gtt ctg gtt att gat att gct aaa cca aat ggg
Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly | 130
135 | 140 | 432 |
| aaa ggg att tca gat aac cgt ttt gaa aaa ttt aat att cca aat agc
Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser | 145
150 | 155
160 | 480 |
| gcg gtg ttt aat aat aat ggg act gaa gca cag gca aga tca aca tta
Ala Val Phe Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu | 165
170 | 175 | 528 |
| att ggt tac att ccg caa aat caa aat tta agg gga ggg aaa gaa gct
Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala | 180
185 | 190 | 576 |
| gat gtt ata tta aat caa gtg aca ggt cct caa gaa agt aaa att gtt
Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val | 195
200 | 205 | 624 |
| ggc gcg ctt gaa gta tta ggt aaa aaa gct gat atc gtc att gca aac
Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn | 210
215 | 220 | 672 |
| caa aat ggt att acc tta aat ggt gta aga aca ata aat tca gat cgt
Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg | 225
230 | 235
240 | 720 |
| ttt gtt gcc act acg agt gag ctt ata gat ccg aat cag atg atg tta
Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu | 245
250 | 255 | 768 |
| aag gtt aca aaa gga aat gtg atc att gat att gat ggt ttt tcg aca
Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr | 260
265 | 270 | 816 |
| gat gga tta aag tat tta gat att att gct aaa aaa att gaa caa aag | | | 864 |

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Asp | Gly | Leu | Lys | Tyr | Leu | Asp | Ile | Ile | Ala | Lys | Ile | Glu | Gln | Lys | 275 | 280 | 285 | | |
| caa | tca | att | aca | tca | ggg | gat | aat | tca | gaa | gca | aaa | aca | gat | gtc | act | 290 | 295 | 300 | 912 |
| Gln | Ser | Ile | Thr | Ser | Gly | Asp | Asn | Ser | Glu | Ala | Lys | Thr | Asp | Val | Thr | | | | |
| ctt | att | gcg | ggt | tcc | agt | gaa | tat | gat | tta | agc | aaa | cat | gag | ctg | aaa | 305 | 310 | 315 | 960 |
| Leu | Ile | Ala | Gly | Ser | Ser | Glu | Tyr | Asp | Leu | Ser | Lys | His | Glu | Leu | Lys | | | | |
| aaa | acg | acg | ggt | gaa | aat | gta | tct | aat | gat | gtt | att | gct | atc | acg | gga | 325 | 330 | 335 | 1008 |
| Lys | Thr | Ser | Gly | Glu | Asn | Val | Ser | Asn | Asp | Val | Ile | Ala | Ile | Thr | Gly | | | | |
| tct | agt | aca | ggc | gca | atg | cat | ggt | aaa | aat | att | aag | ttg | att | gtg | aca | 340 | 345 | 350 | 1056 |
| Ser | Ser | Thr | Gly | Ala | Met | His | Gly | Lys | Asn | Ile | Lys | Leu | Ile | Val | Thr | | | | |
| gat | aaa | ggt | gca | ggc | gta | aaa | cat | gat | gga | att | att | ttg | tct | gaa | aat | 355 | 360 | 365 | 1104 |
| Asp | Lys | Gly | Ala | Gly | Val | Lys | His | Asp | Gly | Ile | Ile | Leu | Ser | Glu | Asn | | | | |
| gat | att | cag | att | gaa | atg | aat | gaa | ggt | gac | tta | gaa | ctt | ggc | aat | acg | 370 | 375 | 380 | 1152 |
| Asp | Ile | Gln | Ile | Glu | Met | Asn | Glu | Gly | Asp | Leu | Glu | Leu | Gly | Asn | Thr | | | | |
| att | cag | caa | aca | gtg | gta | aaa | aaa | gac | cga | aat | att | cga | gcc | aag | aaa | 385 | 390 | 395 | 1200 |
| Ile | Gln | Gln | Thr | Val | Val | Lys | Lys | Asp | Arg | Asn | Ile | Arg | Ala | Lys | Lys | | | | |
| aaa | att | gaa | gtg | aaa | aac | gct | aat | cgt | gtt | ttt | gtt | ggt | agt | caa | acg | 405 | 410 | 415 | 1248 |
| Lys | Ile | Glu | Val | Lys | Asn | Ala | Asn | Arg | Val | Phe | Val | Gly | Ser | Gln | Thr | | | | |
| aaa | tca | gat | gaa | att | tgc | tta | gag | gcg | aaa | caa | gtt | aaa | atc | aga | aaa | 420 | 425 | 430 | 1296 |
| Lys | Ser | Asp | Glu | Ile | Ser | Leu | Glu | Ala | Lys | Gln | Val | Lys | Ile | Arg | Lys | | | | |
| aac | gca | gag | att | agg | agt | acg | aca | caa | gcc | aaa | atc | gta | gca | aag | ggt | 435 | 440 | 445 | 1344 |
| Asn | Ala | Glu | Ile | Arg | Ser | Thr | Thr | Gln | Ala | Lys | Ile | Val | Ala | Lys | Gly | | | | |
| gcc | ctg | tct | att | gag | caa | aat | gcg | aag | ctc | gtc | gct | aaa | aag | ata | gat | 450 | 455 | 460 | 1392 |
| Ala | Leu | Ser | Ile | Glu | Gln | Asn | Ala | Lys | Leu | Val | Ala | Lys | Lys | Ile | Asp | | | | |
| gtg | gca | aca | gaa | act | cta | act | aat | gct | ggg | cgt | att | tat | gtt | cga | gag | 465 | 470 | 475 | 1440 |
| Val | Ala | Thr | Glu | Thr | Leu | Thr | Asn | Ala | Gly | Arg | Ile | Tyr | Gly | Arg | Glu | | | | |
| gtt | aag | ctt | gac | act | aat | ttg | att | aat | gat | aaa | gaa | att | tat | gct | | 485 | 490 | 495 | 1488 |
| Val | Lys | Leu | Asp | Thr | Asn | Asn | Leu | Ile | Asn | Asp | Lys | Glu | Ile | Tyr | Ala | | | | |
| gaa | cg | aaa | ttg | agt | att | ttg | acg | aaa | gga | aaa | gat | ctt | gaa | att | att | 500 | 505 | 510 | 1536 |
| Glu | Arg | Lys | Leu | Ser | Ile | Leu | Thr | Lys | Gly | Lys | Asp | Leu | Glu | Ile | Ile | | | | |
| caa | gat | aga | tat | ttg | tct | cca | ctg | atg | cgc | gta | aaa | agt | agt | gtc | cgc | 515 | 520 | 525 | 1584 |
| Gln | Asp | Arg | Tyr | Leu | Ser | Pro | Leu | Met | Arg | Val | Lys | Ser | Ser | Val | Arg | | | | |

| | |
|---|------|
| ttt tta ggc tct ccg ttt ttc tca ata tct ccg tcg atg ctc gca agc
Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser
530 535 540 | 1632 |
| ctt agt gca cag ttt aag cct ggt ttt gtg aat aag gga ctc att gaa
Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu
545 550 555 560 | 1680 |
| agt gcg ggg agt gca gaa tta act ttt aaa gaa aaa acc agt ttt tta
Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu
565 570 575 | 1728 |
| aca gag ggc aat aat ttt att aga gct aaa gat gcg tta act att aac
Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn
580 585 590 | 1776 |
| gcc caa aat att gaa att gat aaa aat caa gat att caa ttg ggt gct
Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala
595 600 605 | 1824 |
| aat ata acg ttg aat gtg gaa gaa aac ttt gtt aat cgt gca gga aca
Asn Ile Thr Leu Asn Val Glu Asn Phe Val Asn Arg Ala Gly Thr
610 615 620 | 1872 |
| ctg gca act ggt aaa aca ctg aca att aat acc gaa agt ggc agt att
Leu Ala Thr Gly Lys Thr Leu Thr Ile Asn Thr Glu Ser Gly Ser Ile
625 630 635 640 | 1920 |
| tac aat ctt ggt ggg aca tta ggt gct gga aaa tca tta aaa ctg act
Tyr Asn Leu Gly Gly Thr Leu Gly Ala Gly Lys Ser Leu Lys Leu Thr
645 650 655 | 1968 |
| gct aaa tca acg gaa gaa ggt atg gga aat att gtt aac caa gaa aac
Ala Lys Ser Thr Glu Glu Gly Met Gly Asn Ile Val Asn Gln Glu Asn
660 665 670 | 2016 |
| ggg tta ttc cat aca ctc ggt aat atg atg tta gaa gca gag cgt tct
Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser
675 680 685 | 2064 |
| gtt tat aat att ggc gat att tat gcg agt aaa aaa tta aca gtt cat
Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr Val His
690 695 700 | 2112 |
| act cat aat ttg att aat gat gtg cgt tta tct ggc aat gtg agt tat
Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr
705 710 715 720 | 2160 |
| aag cct atc ggt tca agt cgt gat tat gat atc agt cgt gtt gcg gta
Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val
725 730 735 | 2208 |
| cat ggt tgg cac aat aat gtt tat aag ctc aac tta aat ctg caa gaa
His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Gln Glu
740 745 750 | 2256 |
| caa gat aaa acc gat att aaa gtt gtg aaa atg ggg gct atc cgt tct
Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser
755 760 765 | 2304 |
| gat ggt gat ttt gac ttt aag gga ata aag gcg aca tca tca gaa tca
Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser
770 775 780 | 2352 |

| | | |
|---|------|------|
| aaa ccg cag tta att aat cat gga tta att aat gtc aaa gga aca ttt | | 2400 |
| Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe | | |
| 785 | 790 | 795 |
| | | 800 |
| aat gcg gaa gct gat caa gtg gtg aac caa atg aaa gcg ttt aac caa | | 2448 |
| Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe Asn Gln | | |
| 805 | 810 | 815 |
| aat gca tta gca agc gtg ttt aag aat cca gcg aaa atc acg atg tac | | 2496 |
| Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr | | |
| 820 | 825 | 830 |
| tat caa cca ctt act cgt tat att tgg aca cca tta tcg ggt aat gca | | 2544 |
| Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly Asn Ala | | |
| 835 | 840 | 845 |
| tcg cgt gaa ttt aac aat tta gag tct ttc ctc gat gcc ttg ttt ggc | | 2592 |
| Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu Phe Gly | | |
| 850 | 855 | 860 |
| tca aca aca atc tta aaa tca agt ttc tat agt acg gaa aat ttt agt | | 2640 |
| Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser | | |
| 865 | 870 | 875 |
| | | 880 |
| gct tat cag ctt cta tct cat att cag cat tca cca atg tac caa aaa | | 2688 |
| Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr Gln Lys | | |
| 885 | 890 | 895 |
| gcg atg gca caa gtg ttt ggt gca gag tgg cat agt aaa tcc tat gat | | 2736 |
| Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp | | |
| 900 | 905 | 910 |
| gag atg cga aac aaa tgg aaa agc ttt aaa gaa aat cca aca gat ttc | | 2784 |
| Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr Asp Phe | | |
| 915 | 920 | 925 |
| att tat tac cca tca gaa aaa gca aaa atc cta gcg gga aaa cta gaa | | 2832 |
| Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu | | |
| 930 | 935 | 940 |
| ggt aag ctt aca acg cta caa aat ggt gaa tat gcc gaa cgt ggt aag | | 2880 |
| Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys | | |
| 945 | 950 | 955 |
| | | 960 |
| ttt gat gag agt atc caa att ggt aaa cac caa tta tcg cta cca tca | | 2928 |
| Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser | | |
| 965 | 970 | 975 |
| gta gag ctt aaa gcg gag ttt agt gat aaa gaa cgt ttg gaa gag gac | | 2976 |
| Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Glu Asp | | |
| 980 | 985 | 990 |
| ggg gta gat tta tcc tcg atc gcc gaa ctc tta gaa atg cca aac tta | | 3024 |
| Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu | | |
| 995 | 1000 | 1005 |
| ttt att gat aat agt atc caa tta gaa aag aaa aag ttg tct cct att | | 3072 |
| Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu Ser Pro Ile | | |
| 1010 | 1015 | 1020 |
| gag gat cta gat gaa gaa cca cgt aaa aat ctg gat ata gaa gaa agc | | 3120 |
| Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser | | |
| 1025 | 1030 | 1035 |
| | | 1040 |

| | |
|---|------|
| cat tct aat tca tcg gat gac gtg ctt agc atg aat gat gat gag tct | 3168 |
| His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp Glu Ser | |
| 1045 1050 1055 | |
| gat aca gac gat agc aag tgg agt atg ggc aat gat gag aaa gag atg | 3216 |
| Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met | |
| 1060 1065 1070 | |
| ccc gat gat aag ctg ggt ata agt cgt gat gat cgt gga aat aaa cca | 3264 |
| Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro | |
| 1075 1080 1085 | |
| cct cgt act gat cct aca gtt gat tat ctt aac cct gat gaa ttc ttt | 3312 |
| Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe | |
| 1090 1095 1100 | |
| gaa aat ggt tat ctc ttg aat gag cta cta cag gag ctt gga gaa gag | 3360 |
| Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly Glu Glu | |
| 1105 1110 1115 1120 | |
| ccg tta cta aaa gaa ggg gaa gat cat ttt aaa cgt tct acc aat cta | 3408 |
| Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu | |
| 1125 1130 1135 | |
| gtc cgt cta ggc gag aga gat agg caa aat aga gaa aag aga gaa aaa | 3456 |
| Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys | |
| 1140 1145 1150 | |
| gag ggg tat ttt gat ctg cct ggt aca tta gat atg aaa ctg cag gag | 3504 |
| Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Gln Glu | |
| 1155 1160 1165 | |
| tta ttc gaa aaa aga aaa caa aaa cac gaa gca gaa cag aaa gca aga | 3552 |
| Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys Ala Arg | |
| 1170 1175 1180 | |
| ata gaa aaa gca ctt cta caa aaa tca gaa caa caa gaa aaa cgt gtt | 3600 |
| Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu Lys Arg Val | |
| 1185 1190 1195 1200 | |
| gaa gaa cgt aag caa gag gaa aaa cgt caa gcg caa gat aaa att gct | 3648 |
| Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys Ile Ala | |
| 1205 1210 1215 | |
| aag caa gta gaa att gca aaa gaa atg caa cgg gta gaa gaa att cgc | 3696 |
| Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu Ile Arg | |
| 1220 1225 1230 | |
| cag aga gaa aaa caa ctt gcg atc caa ctg caa gaa gaa gag aag aaa | 3744 |
| Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Lys Lys | |
| 1235 1240 1245 | |
| caa caa gaa gaa aaa cat tta tcc gag gag aaa aaa caa gct gaa cag | 3792 |
| Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln Ala Glu Gln | |
| 1250 1255 1260 | |
| aaa caa aaa gct gag gag aaa gtt gca caa gaa aga tta gac att gaa | 3840 |
| Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu Asp Ile Glu | |
| 1265 1270 1275 1280 | |
| caa cag aaa gcg tat gaa gaa atg gcg aag cga gag gca gag gca tca | 3888 |
| Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala Glu Ala Ser | |
| 1285 1290 1295 | |

| | |
|---|------|
| aaa aat gtt tta ttg aaa gcg att gat gaa gaa cgt cca aaa gtg gaa | 3936 |
| Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro Lys Val Glu | |
| 1300 1305 1310 | |
| act gat cca ctt ttc cgt aca aaa ttg aaa tat atc aat caa gat gac | 3984 |
| Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp | |
| 1315 1320 1325 | |
| tat gct ggt gca aat tat ttc ttc aat aaa gtt ggt tta aat aca aaa | 4032 |
| Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn Thr Lys | |
| 1330 1335 1340 | |
| ggt cat caa aaa gta aat gtg tta ggg gat aac tat ttt gat cat caa | 4080 |
| Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln | |
| 1345 1350 1355 1360 | |
| gtg att act cgc tcg att gag aaa aaa gta gat aac cac ctt aac caa | 4128 |
| Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln | |
| 1365 1370 1375 | |
| aaa tac aat ctc agc gat gtg gaa tta gtt aaa cag ctg atg gac aat | 4176 |
| Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn | |
| 1380 1385 1390 | |
| tcc aca aca caa gcg cag gag ttg gat ttg aaa cta ggt gcg gca tta | 4224 |
| Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala Ala Leu | |
| 1395 1400 1405 | |
| act aaa gaa caa caa gct aac ttg acc caa gat atc gtt tgg tat gtc | 4272 |
| Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp Tyr Val | |
| 1410 1415 1420 | |
| aaa acg aag gta aag ggc aaa gat gtg ttt gtt cca aag gtt tat ttc | 4320 |
| Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe | |
| 1425 1430 1435 1440 | |
| gct tct gaa acg ctc gta gaa gcc caa aaa tta caa ggt tta ggc act | 4368 |
| Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly Leu Gly Thr | |
| 1445 1450 1455 | |
| ggg act atc aga gtt ggt gaa gct aag att aaa gcc aaa gat gtg gtg | 4416 |
| Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val | |
| 1460 1465 1470 | |
| aat acc ggg aca tta gct ggg aga aaa ctc aat gtt gaa gcg agt aat | 4464 |
| Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn | |
| 1475 1480 1485 | |
| aaa atc aaa aat caa ggg agt atc tta agt act caa gaa aca cgt tta | 4512 |
| Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr Arg Leu | |
| 1490 1495 1500 | |
| gtc ggg cgt aaa ggt att gaa aac gta tct cgt tca ttt gca aat gat | 4560 |
| Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp | |
| 1505 1510 1515 1520 | |
| gaa tta gga gtc act gca caa cgc tca gaa atc aaa acg gaa ggt cat | 4608 |
| Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His | |
| 1525 1530 1535 | |
| tta cat ctt gaa aca gat aag gat tca act att gat gta caa gca tcg | 4656 |
| Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser | |
| 1540 1545 1550 | |

| | | | |
|---|-----------------|------|------|
| gat att aaa gca aaa aca agc ttt gtg aag act ggt gat | gtg aat ctc | 4704 | |
| Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp | Val Asn Leu | | |
| 1555 | 1560 | 1565 | |
| aaa aat aca tac aat act aaa cat gcc tac cgt gag | aaa ttc tcg ccg | 4752 | |
| Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu | Lys Phe Ser Pro | | |
| 1570 | 1575 | 1580 | |
| agt gca cta caa gtt gca gaa ctt gat gtg gca ggg ctt aaa gtc cca | 4800 | | |
| Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro | | | |
| 1585 | 1590 | 1595 | 1600 |
| ctt tta ggc gtg tcc gtc tcc atc cag ttt att cag agc ata cta gtg | 4848 | | |
| Leu Leu Gly Val Ser Val Ser Ile Gln Phe Ile Gln Ser Ile Leu Val | | | |
| 1605 | 1610 | 1615 | |
| agg caa ctt caa gag gga tca atc ttc gaa gta ggg cac tta cat ntt | 4896 | | |
| Arg Gln Leu Gln Glu Gly Ser Ile Phe Glu Val Gly His Leu His Xaa | | | |
| 1620 | 1625 | 1630 | |
| gcg gta gac aga aga tgt gaa cca agc ggg gag ta | 4931 | | |
| Ala Val Asp Arg Arg Cys Glu Pro Ser Gly Glu | | | |
| 1635 | 1640 | | |

<210> 103

<211> 1643

<212> PRT

<213> Pasteurella multocida

<220>

<221> misc_feature

<222> 1632

<223> Xaa = any or unknown amino acid

<400> 103

| | | | |
|---|---|----|----|
| Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Gln Val Lys Gly Cys | | | |
| 1 | 5 | 10 | 15 |

| | | |
|---|----|----|
| Leu Val Pro Val Ala Glu Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser | | |
| 20 | 25 | 30 |

| | | |
|---|----|----|
| Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Pro Phe Leu | | |
| 35 | 40 | 45 |

| | | |
|---|----|----|
| Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr | | |
| 50 | 55 | 60 |

| | | | |
|---|----|----|----|
| Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser | | | |
| 65 | 70 | 75 | 80 |

| | | |
|---|----|----|
| Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys | | |
| 85 | 90 | 95 |

| | | |
|---|-----|-----|
| Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile | | |
| 100 | 105 | 110 |

| | | |
|---|-----|-----|
| Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr | | |
| 115 | 120 | 125 |

| | | |
|---|-----|-----|
| Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly | | |
| 130 | 135 | 140 |

Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser
 145 150 155 160
 Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu
 165 170 175
 Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala
 180 185 190
 Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val
 195 200 205
 Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn
 210 215 220
 Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg
 225 230 235 240
 Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu
 245 250 255
 Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr
 260 265 270
 Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys
 275 280 285
 Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr
 290 295 300
 Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys
 305 310 315 320
 Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly
 325 330 335
 Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr
 340 345 350
 Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn
 355 360 365
 Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr
 370 375 380
 Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys
 385 390 395 400
 Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr
 405 410 415
 Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys
 420 425 430
 Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly
 435 440 445
 Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp
 450 455 460
 Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu
 465 470 475 480

Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala
 485 490 495

 Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile
 500 505 510

 Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg
 515 520 525

 Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser
 530 535 540

 Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu
 545 550 555 560

 Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu
 565 570 575

 Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn
 580 585 590

 Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala
 595 600 605

 Asn Ile Thr Leu Asn Val Glu Glu Asn Phe Val Asn Arg Ala Gly Thr
 610 615 620

 Leu Ala Thr Gly Lys Thr Leu Thr Ile Asn Thr Glu Ser Gly Ser Ile
 625 630 635 640

 Tyr Asn Leu Gly Gly Thr Leu Gly Ala Gly Lys Ser Leu Lys Leu Thr
 645 650 655

 Ala Lys Ser Thr Glu Glu Gly Met Gly Asn Ile Val Asn Gln Glu Asn
 660 665 670

 Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser
 675 680 685

 Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr Val His
 690 695 700

 Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr
 705 710 715 720

 Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val
 725 730 735

 His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu
 740 745 750

 Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser
 755 760 765

 Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser
 770 775 780

 Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe
 785 790 795 800

 Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe Asn Gln
 805 810 815

Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr
 820 825 830
 Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly Asn Ala
 835 840 845
 Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu Phe Gly
 850 855 860
 Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser
 865 870 875 880
 Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr Gln Lys
 885 890 895
 Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp
 900 905 910
 Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr Asp Phe
 915 920 925
 Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu
 930 935 940
 Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys
 945 950 955 960
 Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser
 965 970 975
 Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Glu Asp
 980 985 990
 Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu
 995 1000 1005
 Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu Ser Pro Ile
 1010 1015 1020
 Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser
 1025 1030 1035 1040
 His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp Glu Ser
 1045 1050 1055
 Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met
 1060 1065 1070
 Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro
 1075 1080 1085
 Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe
 1090 1095 1100
 Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly Glu Glu
 1105 1110 1115 1120
 Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu
 1125 1130 1135
 Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys
 1140 1145 1150

Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Gln Glu
 1155 1160 1165
 Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys Ala Arg
 1170 1175 1180
 Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu Lys Arg Val
 1185 1190 1195 1200
 Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys Ile Ala
 1205 1210 1215
 Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu Ile Arg
 1220 1225 1230
 Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Glu Lys Lys
 1235 1240 1245
 Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln Ala Glu Gln
 1250 1255 1260
 Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu Asp Ile Glu
 1265 1270 1275 1280
 Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala Glu Ala Ser
 1285 1290 1295
 Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro Lys Val Glu
 1300 1305 1310
 Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp
 1315 1320 1325
 Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn Thr Lys
 1330 1335 1340
 Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln
 1345 1350 1355 1360
 Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln
 1365 1370 1375
 Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn
 1380 1385 1390
 Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala Ala Leu
 1395 1400 1405
 Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp Tyr Val
 1410 1415 1420
 Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe
 1425 1430 1435 1440
 Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly Leu Gly Thr
 1445 1450 1455
 Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val
 1460 1465 1470
 Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn
 1475 1480 1485

Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr Arg Leu
 1490 1495 1500
 Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp
 1505 1510 1515 1520
 Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His
 1525 1530 1535
 Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser
 1540 1545 1550
 Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val Asn Leu
 1555 1560 1565
 Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe Ser Pro
 1570 1575 1580
 Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro
 1585 1590 1595 1600
 Leu Leu Gly Val Ser Val Ser Ile Gln Phe Ile Gln Ser Ile Leu Val
 1605 1610 1615
 Arg Gln Leu Gln Glu Gly Ser Ile Phe Glu Val Gly His Leu His Xaa
 1620 1625 1630
 Ala Val Asp Arg Arg Cys Glu Pro Ser Gly Glu
 1635 1640

<210> 104
 <211> 2009
 <212> DNA
 <213> Pasteurella multocida

<220>
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<220>
 <221> CDS
 <222> (1)..(2007)

<400> 104
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 Ile Arg Gly Val Asp Lys Asp Arg Val Ala Val Ile Val Asp Gly Ile
 1 5 10 15
 ccg cag gct gaa tcg act ata tct act tcc gca cgt tat tcg act gaa 96
 Pro Gln Ala Glu Ser Thr Ile Ser Thr Ser Ala Arg Tyr Ser Thr Glu
 20 25 30
 cgt cat aat ggt aat att aat aat att gaa tac gaa aat gtt agt tcg 144
 Arg His Asn Gly Asn Ile Asn Asn Ile Glu Tyr Glu Asn Val Ser Ser
 35 40 45
 ttg aaa gtt caa aaa ggg gca gct tct gta atg tat ggt agc ggt gcg 192
 Leu Lys Val Gln Lys Gly Ala Ala Ser Val Met Tyr Gly Ser Gly Ala
 50 55 60
 tta ggt gga acc gtg gag ttt acc aca aaa gat att gag gac ttt gtc 240
 Leu Gly Gly Thr Val Glu Phe Thr Thr Lys Asp Ile Glu Asp Phe Val
 65 70 75 80

| | |
|---|------|
| gaa cct ggt cgc cat ttg ggc ttt ttg tct aaa acc ggc tat act tca | 288 |
| Glu Pro Gly Arg His Leu Gly Phe Leu Ser Lys Thr Gly Tyr Thr Ser | |
| 85 90 95 | |
| aaa aac aga gaa tat cgt caa gtc atc gga gtt gga ggg aaa ggg gaa | 336 |
| Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Gly Lys Gly Glu | |
| 100 105 110 | |
| cac ttt ttt ggt ttt gta caa tta acc aaa cgt tgg ggg cat gaa aca | 384 |
| His Phe Phe Gly Phe Val Gln Leu Thr Lys Arg Trp Gly His Glu Thr | |
| 115 120 125 | |
| atc aac aac ggc aaa ggt aca gac att ctc ggc gaa cat cga ggt aaa | 432 |
| Ile Asn Asn Gly Lys Gly Thr Asp Ile Leu Gly His Arg Gly Lys | |
| 130 135 140 | |
| ccc aat ccg ctc aac tac tat act aca tca tgg tta acg aaa gtc ggt | 480 |
| Pro Asn Pro Leu Asn Tyr Tyr Thr Ser Trp Leu Thr Lys Val Gly | |
| 145 150 155 160 | |
| tac gat att aat aac act cat cgt ttt aca ctg ttt tta gaa gat cgc | 528 |
| Tyr Asp Ile Asn Asn Thr His Arg Phe Leu Phe Leu Glu Asp Arg | |
| 165 170 175 | |
| cgt gaa aag aag ctt acc gaa gaa aaa aca tta ggg ctt agt gat gca | 576 |
| Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu Gly Leu Ser Asp Ala | |
| 180 185 190 | |
| gtg cgt ttt gct aat gat caa acc cct tat ctc cgt tat ggt att gaa | 624 |
| Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu Arg Tyr Gly Ile Glu | |
| 195 200 205 | |
| tat cga tat aac ggc ttg tct tgg ttg gaa acg gta aag ctt ttt ttg | 672 |
| Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr Val Lys Leu Phe Leu | |
| 210 215 220 | |
| gca aag cag aaa atc gaa caa cgt tct gct ctc caa gag ttt gat att | 720 |
| Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu Gln Glu Phe Asp Ile | |
| 225 230 235 240 | |
| aat aat agg aat aaa ttg gat tcg act atg tcg ttt gta tat tta caa | 768 |
| Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser Phe Val Tyr Leu Gln | |
| 245 250 255 | |
| aga cag aat ata gct cgg gga gaa ttt tca acg agt cct tta tat ttg | 816 |
| Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr Ser Pro Leu Tyr Trp | |
| 260 265 270 | |
| ggg ccg agt cgc cat cgt tta tct gcg aaa ttc gaa ttt cgt gat aag | 864 |
| Gly Pro Ser Arg His Arg Leu Ser Ala Lys Phe Glu Phe Arg Asp Lys | |
| 275 280 285 | |
| ttt tta gaa aat atg aat aag cat ttt acg ttt cgg ccg ttg caa atc | 912 |
| Phe Leu Glu Asn Met Asn Lys His Phe Thr Phe Arg Pro Trp Gln Ile | |
| 290 295 300 | |
| aat aga ttc aga caa caa ggt cga aat aac tat aca gaa gtg ttt ccc | 960 |
| Asn Arg Phe Arg Gln Gln Gly Arg Asn Asn Tyr Thr Glu Val Phe Pro | |
| 305 310 315 320 | |
| gtt aaa tcc cga gag ttt tct ttt ctt atg gac gac att aag att | 1008 |
| Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met Asp Asp Ile Lys Ile | |
| 325 330 335 | |

| | |
|---|------|
| ggc gaa ttg cta cat ctc gga ttg ggc ggt cgg tgg gat cac tat aac
Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg Trp Asp His Tyr Asn
340 345 350 | 1056 |
| tat aag cca tta tta aat tct cag cat aat atc aac agg aca cag aga
Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile Asn Arg Thr Gln Arg
355 360 365 | 1104 |
| tta cct tat cca aaa aca tca tcc aaa ttt tcg tat caa ttg agt tta
Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser Tyr Gln Leu Ser Leu
370 375 380 | 1152 |
| gag tat caa tta cat cca tca cat caa att gca tac cgt tta agt acc
Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala Tyr Arg Leu Ser Thr
385 390 395 400 | 1200 |
| ggg ttt agg gtt ccc cgt gtt gaa gat ctt tat ttt gaa gac cga gga
Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr Phe Glu Asp Arg Gly
405 410 415 | 1248 |
| aaa agt tct tca caa ttt ctt cct aac ccc gat cta caa ccg gaa act
Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp Leu Gln Pro Glu Thr
420 425 430 | 1296 |
| gca ctg aat cat gaa ata agt tac cgt ttc caa aat caa tat gcc cat
Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln Asn Gln Tyr Ala His
435 440 445 | 1344 |
| ttc agc gtc ggg ctt ttc cgt aca cgt tat cat aac ttt att caa gaa
Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His Asn Phe Ile Gln Glu
450 455 460 | 1392 |
| cgt gag atg acc tgt gat aaa att cca tat gag tat aat agg act tat
Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu Tyr Asn Arg Thr Tyr
465 470 475 480 | 1440 |
| gga tat tgc acg cat aat act tat gta atg ttt gtt aat gaa cct gaa
Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe Val Asn Glu Pro Glu
485 490 495 | 1488 |
| gcc gtg att aaa ggg gtt gaa gta agc ggt gct tta aat ggg tcg gca
Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala Leu Asn Gly Ser Ala
500 505 510 | 1536 |
| ttc gga ctt tcc gac ggt tta act ttc cgt ctc aaa ggg agc tac agc
Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu Lys Gly Ser Tyr Ser
515 520 525 | 1584 |
| aaa ggt caa aat cat gac ggc gat ccg tta aaa tct att caa cca tgg
Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys Ser Ile Gln Pro Trp
530 535 540 | 1632 |
| aca gtg gta acc ggt att gat tac gaa act gaa ggg tgg agc gtg agt
Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu Gly Trp Ser Val Ser
545 550 555 560 | 1680 |
| ttg agc ggg cgt tat agt gct aaa aaa gcc aaa gat gcg ata gaa
Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala Lys Asp Ala Ile Glu
565 570 575 | 1728 |
| acg gaa tac aca cat gat aaa aag gtt gtc aaa caa tgg ccg cat tta
Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys Gln Trp Pro His Leu
580 585 590 | 1776 |

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|---|------|
| agt cca tcc tac ttt gtt gat ttt acg ggg caa gtt aac ctc agt
Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly Gln Val Asn Leu Ser
595 600 605 | 1824 |
| aaa aat gtc att ttg aat atg ggg gta ttt aac ttg ttc aat cgt gat
Lys Asn Val Ile Leu Asn Met Gly Val Phe Asn Leu Phe Asn Arg Asp
610 615 620 | 1872 |
| tat atg acg tgg gac agt gca tat aac ttg ttt act agg ggg tat act
Tyr Met Thr Trp Asp Ser Ala Tyr Asn Leu Phe Thr Arg Gly Tyr Thr
625 630 635 640 | 1920 |
| tcc cgt tct gtc cgt gct aac agc cca ggc att aat cgg ttt acc gca
Ser Arg Ser Val Arg Ala Asn Ser Pro Gly Ile Asn Arg Phe Thr Ala
645 650 655 | 1968 |
| cca aaa cgt aat ttt gct gcc tcg gtg gaa att cgt ttt ta
Pro Lys Arg Asn Phe Ala Ala Ser Val Glu Ile Arg Phe
660 665 | 2009 |
|
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| <210> 105 | |
| <211> 669 | |
| <212> PRT | |
| <213> Pasteurella multocida | |
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| <400> 105 | |
| Ile Arg Gly Val Asp Lys Asp Arg Val Ala Val Ile Val Asp Gly Ile
1 5 10 15 | |
| Pro Gln Ala Glu Ser Thr Ile Ser Thr Ser Ala Arg Tyr Ser Thr Glu
20 25 30 | |
| Arg His Asn Gly Asn Ile Asn Asn Ile Glu Tyr Glu Asn Val Ser Ser
35 40 45 | |
| Leu Lys Val Gln Lys Gly Ala Ala Ser Val Met Tyr Gly Ser Gly Ala
50 55 60 | |
| Leu Gly Gly Thr Val Glu Phe Thr Thr Lys Asp Ile Glu Asp Phe Val
65 70 75 80 | |
| Glu Pro Gly Arg His Leu Gly Phe Leu Ser Lys Thr Gly Tyr Thr Ser
85 90 95 | |
| Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Lys Gly Glu
100 105 110 | |
| His Phe Phe Gly Phe Val Gln Leu Thr Lys Arg Trp Gly His Glu Thr
115 120 125 | |
| Ile Asn Asn Gly Lys Gly Thr Asp Ile Leu Gly Glu His Arg Gly Lys
130 135 140 | |
| Pro Asn Pro Leu Asn Tyr Tyr Thr Ser Trp Leu Thr Lys Val Gly
145 150 155 160 | |
| Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu Phe Leu Glu Asp Arg
165 170 175 | |
| Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu Gly Leu Ser Asp Ala
180 185 190 | |

Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu Arg Tyr Gly Ile Glu
 195 200 205
 Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr Val Lys Leu Phe Leu
 210 215 220
 Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu Gln Glu Phe Asp Ile
 225 230 235 240
 Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser Phe Val Tyr Leu Gln
 245 250 255
 Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr Ser Pro Leu Tyr Trp
 260 265 270
 Gly Pro Ser Arg His Arg Leu Ser Ala Lys Phe Glu Phe Arg Asp Lys
 275 280 285
 Phe Leu Glu Asn Met Asn Lys His Phe Thr Phe Arg Pro Trp Gln Ile
 290 295 300
 Asn Arg Phe Arg Gln Gln Gly Arg Asn Asn Tyr Thr Glu Val Phe Pro
 305 310 315 320
 Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met Asp Asp Ile Lys Ile
 325 330 335
 Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg Trp Asp His Tyr Asn
 340 345 350
 Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile Asn Arg Thr Gln Arg
 355 360 365
 Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser Tyr Gln Leu Ser Leu
 370 375 380
 Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala Tyr Arg Leu Ser Thr
 385 390 395 400
 Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr Phe Glu Asp Arg Gly
 405 410 415
 Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp Leu Gln Pro Glu Thr
 420 425 430
 Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln Asn Gln Tyr Ala His
 435 440 445
 Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His Asn Phe Ile Gln Glu
 450 455 460
 Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu Tyr Asn Arg Thr Tyr
 465 470 475 480
 Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe Val Asn Glu Pro Glu
 485 490 495
 Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala Leu Asn Gly Ser Ala
 500 505 510
 Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu Lys Gly Ser Tyr Ser
 515 520 525

Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys Ser Ile Gln Pro Trp
 530 535 540

Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu Gly Trp Ser Val Ser
 545 550 555 560

Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala Lys Asp Ala Ile Glu
 565 570 575

Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys Gln Trp Pro His Leu
 580 585 590

Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly Gln Val Asn Leu Ser
 595 600 605

Lys Asn Val Ile Leu Asn Met Gly Val Phe Asn Leu Phe Asn Arg Asp
 610 615 620

Tyr Met Thr Trp Asp Ser Ala Tyr Asn Leu Phe Thr Arg Gly Tyr Thr
 625 630 635 640

Ser Arg Ser Val Arg Ala Asn Ser Pro Gly Ile Asn Arg Phe Thr Ala
 645 650 655

Pro Lys Arg Asn Phe Ala Ala Ser Val Glu Ile Arg Phe
 660 665

<210> 106

<211> 908

<212> DNA

<213> Pasteurella multocida

<220>

<223> lgtC

<220>

<221> CDS

<222> (1)...(906)

<400> 106

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 1 5 10 15

gtt gcg att aaa agc att ata aat cat aat gaa aaa ggt att tca ttt 96
 Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe
 20 25 30

tat att ttt gat ttg ggt ata aag gat gaa aat aag aga aat att aat 144
 Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
 35 40 45

gat att gtt tct tct tat gga agt gaa gtc aac ttt att gct gtg aat 192
 Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
 50 55 60

gag aaa gaa ttt gag agt ttt cct gtt caa att agt tat att tct tta 240
 Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
 65 70 75 80

| | |
|---|-----|
| gca aca tat gca agg cta aaa gcg gca gag tat ttg ccg gat aat tta | 288 |
| Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu | |
| 85 | 90 |
| 95 | |
| aat aaa att att tat tta gat gtt gat ttg gtt ttt aac tca tta | 336 |
| Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu | |
| 100 | 105 |
| 110 | |
| gaa atg tta tgg aat gtt gat gtt aat aat ttt ctt acc gca gcc tgt | 384 |
| Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys | |
| 115 | 120 |
| 125 | |
| tat gat tct ttc atc gaa aat gaa aag tct gag cat aaa aaa tcg att | 432 |
| Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile | |
| 130 | 135 |
| 140 | |
| tca atg tca gat aag gaa tat tat ttt aat gca gga gta atg cta ttt | 480 |
| Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe | |
| 145 | 150 |
| 155 | 160 |
| aat tta gat gaa tgg cg ^g aag atg gat gta ttc tca aga gct tta gac | 528 |
| Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp | |
| 165 | 170 |
| 175 | |
| ctg tta gct atg tat cct aat caa atg att tat cag gat caa gat ata | 576 |
| Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile | |
| 180 | 185 |
| 190 | |
| ttg aat atc ctt ttt agg aat aaa gtc tgt tat tta gat tgc aga ttt | 624 |
| Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe | |
| 195 | 200 |
| 205 | |
| aat ttc atg cca aat caa ctt gaa aga ata aaa caa tac cat aaa gga | 672 |
| Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Lys Gln Tyr His Lys Gly | |
| 210 | 215 |
| 220 | |
| aaa ttg agc aac tta cat tct tta gaa aaa aca acg atg cct gtc gtt | 720 |
| Lys Leu Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val | |
| 225 | 230 |
| 235 | 240 |
| att tca cat tat tgt ggt cca gaa aaa gcg tgg cat gcg gat tgt aaa | 768 |
| Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys | |
| 245 | 250 |
| 255 | |
| cat ttt aat gta tat ttc tat cag aaa ata tta gca gaa ata acg aga | 816 |
| His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Glu Ile Thr Arg | |
| 260 | 265 |
| 270 | |
| ggc acg gat aaa gaa cgc gta tta tct ata aaa act tat ctc aag gcc | 864 |
| Gly Thr Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala | |
| 275 | 280 |
| 285 | |
| ttg att aga agg att aga tat aaa ttc aaa tat caa gtc tat ta | 908 |
| Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr | |
| 290 | 295 |
| 300 | |

<210> 107

<211> 302

<212> PRT

<213> Pasteurella multocida

<400> 107

Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val
 1 5 10 15
 Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe
 20 25 30
 Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
 35 40 45
 Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
 50 55 60
 Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
 65 70 75 80
 Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu
 85 90 95
 Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu
 100 105 110
 Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys
 115 120 125
 Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile
 130 135 140
 Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe
 145 150 155 160
 Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp
 165 170 175
 Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile
 180 185 190
 Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe
 195 200 205
 Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Lys Gln Tyr His Lys Gly
 210 215 220
 Lys Leu Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val
 225 230 235 240
 Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys
 245 250 255
 His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Glu Ile Thr Arg
 260 265 270
 Gly Thr Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala
 275 280 285
 Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr
 290 295 300

<210> 108
 <211> 2054
 <212> DNA
 <213> Pasteurella multocida

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<220>
<221> CDS
<222> (1)..(2052)

<400> 108
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Met Ala Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys
    1           5           10          15

aaa gat gtg aaa gaa ggt caa gac ttc ttc cca tta act gtt aac tat 96
Lys Asp Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asn Tyr
    20          25          30

caa gag cgt act tat gct gca ggc cgt att cct ggt ggc ttt ttc aaa 144
Gln Glu Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Gly Phe Phe Lys
    35          40          45

cgt gaa ggt cgt cct tct gaa ggc gaa act tta att gct cgt tta att 192
Arg Glu Gly Arg Pro Ser Glu Gly Glu Thr Leu Ile Ala Arg Leu Ile
    50          55          60

gac cgt cca att cgt cct ctt ttc cca gaa ggt ttt tat aac gaa atc 240
Asp Arg Pro Ile Arg Pro Leu Phe Pro Glu Gly Phe Tyr Asn Glu Ile
    65          70          75          80

caa atc gtg gcg aca gtg gtg tct gtt aat ccg caa att tgt cca gat 288
Gln Ile Val Ala Thr Val Val Ser Val Asn Pro Gln Ile Cys Pro Asp
    85          90          95

tta gtg gca atg atc ggt gca tct gcg gca ctt tct tta tca ggt gtg 336
Leu Val Ala Met Ile Gly Ala Ser Ala Ala Leu Ser Leu Ser Gly Val
    100         105         110

cca ttt aat ggc cct atc ggt gcg gca cgt gtt ggt ttt att gat gat 384
Pro Phe Asn Gly Pro Ile Gly Ala Ala Arg Val Gly Phe Ile Asp Asp
    115         120         125

caa ttt gtg tta aac cca acc atg aac gag caa aaa caa agc cgt tta 432
Gln Phe Val Leu Asn Pro Thr Met Asn Glu Gln Lys Gln Ser Arg Leu
    130         135         140

gac ttg gtt gtc gcg gga aca gat aaa gcg gtg tta atg gtg gaa tct 480
Asp Leu Val Val Ala Gly Thr Asp Lys Ala Val Leu Met Val Glu Ser
    145         150         155         160

gaa gcc gat gta tta acc gaa gaa caa atg tta gct gcg gtg gtg ttt 528
Glu Ala Asp Val Leu Thr Glu Glu Gln Met Leu Ala Ala Val Val Phe
    165         170         175

ggc cat cag caa caa caa gtg gtg att gac gcg atc aaa gaa ttt acc 576
Gly His Gln Gln Gln Val Val Ile Asp Ala Ile Lys Glu Phe Thr
    180         185         190

gca gaa gcc ggt aaa ccg cgt tgg gat tgg gtg gca cct gaa cca aat 624
Ala Glu Ala Gly Lys Pro Arg Trp Asp Trp Val Ala Pro Glu Pro Asn
    195         200         205

acc gcg tta att gaa aaa gtg aaa gcg att gca gaa gcg cgt tta ggc 672
Thr Ala Leu Ile Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly
    210         215         220

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| | |
|---|------|
| gaa gca tac cgt atc act gaa aaa caa gca cgt tat gaa caa att gat
Glu Ala Tyr Arg Ile Thr Glu Lys Gln Ala Arg Tyr Glu Gln Ile Asp
225 230 235 240 | 720 |
| gcg att aaa gct gat gtg att gca caa atc aca gct gaa gta gca gaa
Ala Ile Lys Ala Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu
245 250 255 | 768 |
| ggc gaa gac atc agt gaa ggg aaa att gtc gat att ttc acc gca ctt
Gly Glu Asp Ile Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu
260 265 270 | 816 |
| gaa agc caa atc gta cgt agc cgt atc att gct ggt gaa cca cgt att
Glu Ser Gln Ile Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile
275 280 285 | 864 |
| gat ggt cgt aca gtg gat act gtt cgt gca tta gat att tgt act ggt
Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly
290 295 300 | 912 |
| gtt tta cca cgt aca cac ggt tct gcg att ttc acc cgt ggt gaa aca
Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr
305 310 315 320 | 960 |
| cag gcg tta gct gtc gcg aca tta ggt aca gaa cgt gat gca caa att
Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile
325 330 335 | 1008 |
| att gat gaa tta aca ggt gag cgt tca gat cac ttc tta ttc cac tac
Ile Asp Glu Leu Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr
340 345 350 | 1056 |
| aac ttc ccg cca tat tct gtg ggt gaa acc ggt atg att ggt tca cca
Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro
355 360 365 | 1104 |
| aaa cgt cgt gaa att ggt cat ggt cgt tta gcg aaa cgc ggt gta gct
Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala
370 375 380 | 1152 |
| gca gtg atg cca aca ctt gcc gag ttc ccg tat gtg gta cgt gtt gtc
Ala Val Met Pro Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val
385 390 395 400 | 1200 |
| tct gaa atc aca gaa tca aat ggt tct tct atg gca tcg gtt tgt
Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Met Ala Ser Val Cys
405 410 415 | 1248 |
| ggt gcg tct tta gca tta atg gat gcg ggt gta cca att aaa gcg gcg
Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala
420 425 430 | 1296 |
| gtt gca ggt att gca atg ggc tta gtc aaa gaa gac gaa aaa ttt gtg
Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val
435 440 445 | 1344 |
| gtg ctt tca gac atc tta ggt gat gaa gat cac tta ggt gac atg gac
Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp
450 455 460 | 1392 |
| ttc aaa gtc gcg ggt aca cgt acg ggt gtg acg gca tta caa atg gat
Phe Lys Val Ala Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp
465 470 475 480 | 1440 |

| | |
|---|------|
| atc aaa atc gaa ggt atc aca gca gaa atc atg caa att gcg tta aac
Ile Lys Ile Glu Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn
485 490 495 | 1488 |
| caa gcg aaa agc gca cgt tta cac att tta ggt gtg atg gag caa gcg
Gln Ala Lys Ser Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala
500 505 510 | 1536 |
| atc cca gcg cca cgt gcg gat att tct gat ttt gca ccg cgt att tac
Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr
515 520 525 | 1584 |
| act atg aaa att gat ccg aag aaa atc aaa gat gtg atc ggt aaa ggt
Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly
530 535 540 | 1632 |
| ggc gca acc att cgt gcc tta aca gaa gaa aca ggt acc tca att gat
Gly Ala Thr Ile Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp
545 550 555 560 | 1680 |
| atc gat gat gat ggt acg gtg aag att gct gcg gtt gat ggc aat tca
Ile Asp Asp Asp Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser
565 570 575 | 1728 |
| gca aaa gag gtg atg gcg cgt att gaa gat att act gca gaa gtt gaa
Ala Lys Glu Val Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu
580 585 590 | 1776 |
| gcg ggt gca gtg tat aaa ggt aaa gtt act cgt tta gct gat ttt ggt
Ala Gly Ala Val Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly
595 600 605 | 1824 |
| gcc ttc gtt tct atc gta ggt aac aaa gaa ggc tta gtg cat att tct
Ala Phe Val Ser Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser
610 615 620 | 1872 |
| caa atc gcg gaa gag cgt gtt gag aaa gtg agt gat tat ctt gca gtg
Gln Ile Ala Glu Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val
625 630 635 640 | 1920 |
| ggg caa gaa gtg act gtt aaa gtg gtt gag att gat cgt caa ggt cgt
Gly Gln Glu Val Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg
645 650 655 | 1968 |
| att cgt tta acc atg aaa gaa gtt gca cca aag caa gaa cac gtt gat
Ile Arg Leu Thr Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp
660 665 670 | 2016 |
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Ser Val Val Ala Asp Val Ala Ala Glu Glu Asn Ala
675 680 | 2054 |
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|---|-----|-----|
| Gln Glu Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Gly Phe Phe Lys | | |
| 35 | 40 | 45 |
| Arg Glu Gly Arg Pro Ser Glu Gly Glu Thr Leu Ile Ala Arg Leu Ile | | |
| 50 | 55 | 60 |
| Asp Arg Pro Ile Arg Pro Leu Phe Pro Glu Gly Phe Tyr Asn Glu Ile | | |
| 65 | 70 | 75 |
| 80 | | |
| Gln Ile Val Ala Thr Val Val Ser Val Asn Pro Gln Ile Cys Pro Asp | | |
| 85 | 90 | 95 |
| Leu Val Ala Met Ile Gly Ala Ser Ala Ala Leu Ser Leu Ser Gly Val | | |
| 100 | 105 | 110 |
| Pro Phe Asn Gly Pro Ile Gly Ala Ala Arg Val Gly Phe Ile Asp Asp | | |
| 115 | 120 | 125 |
| Gln Phe Val Leu Asn Pro Thr Met Asn Glu Gln Lys Gln Ser Arg Leu | | |
| 130 | 135 | 140 |
| Asp Leu Val Val Ala Gly Thr Asp Lys Ala Val Leu Met Val Glu Ser | | |
| 145 | 150 | 155 |
| 160 | | |
| Glu Ala Asp Val Leu Thr Glu Glu Gln Met Leu Ala Ala Val Val Phe | | |
| 165 | 170 | 175 |
| Gly His Gln Gln Gln Val Val Ile Asp Ala Ile Lys Glu Phe Thr | | |
| 180 | 185 | 190 |
| Ala Glu Ala Gly Lys Pro Arg Trp Asp Trp Val Ala Pro Glu Pro Asn | | |
| 195 | 200 | 205 |
| Thr Ala Leu Ile Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly | | |
| 210 | 215 | 220 |
| Glu Ala Tyr Arg Ile Thr Glu Lys Gln Ala Arg Tyr Glu Gln Ile Asp | | |
| 225 | 230 | 235 |
| 240 | | |
| Ala Ile Lys Ala Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu | | |
| 245 | 250 | 255 |
| Gly Glu Asp Ile Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu | | |
| 260 | 265 | 270 |
| Glu Ser Gln Ile Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile | | |
| 275 | 280 | 285 |
| Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly | | |
| 290 | 295 | 300 |
| Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr | | |
| 305 | 310 | 315 |
| 320 | | |
| Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile | | |
| 325 | 330 | 335 |
| Ile Asp Glu Leu Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr | | |
| 340 | 345 | 350 |
| Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro | | |

| 355 | 360 | 365 | |
|---|-------------------------|-----------------|-----|
| Lys Arg Arg Glu Ile Gly His | Gly Arg Leu Ala Lys | Arg Gly Val Ala | |
| 370 | 375 | 380 | |
| Ala Val Met Pro Thr Leu Ala Glu Phe Pro | Tyr Val Val Arg Val | Val | |
| 385 | 390 | 395 | 400 |
| Ser Glu Ile Thr Glu Ser Asn Gly Ser | Ser Ser Met Ala Ser | Val Cys | |
| 405 | 410 | 415 | |
| Gly Ala Ser Leu Ala Leu Met Asp Ala | Gly Val Pro Ile Lys | Ala Ala | |
| 420 | 425 | 430 | |
| Val Ala Gly Ile Ala Met Gly Leu Val Lys | Glu Asp Glu Lys | Phe Val | |
| 435 | 440 | 445 | |
| Val Leu Ser Asp Ile Leu Gly Asp Glu Asp | His Leu Gly Asp Met Asp | | |
| 450 | 455 | 460 | |
| Phe Lys Val Ala Gly Thr Arg Thr Gly Val | Thr Ala Leu Gln Met Asp | | |
| 465 | 470 | 475 | 480 |
| Ile Lys Ile Glu Gly Ile Thr Ala Glu Ile | Met Gln Ile Ala Leu Asn | | |
| 485 | 490 | 495 | |
| Gln Ala Lys Ser Ala Arg Leu His Ile Leu Gly Val | Met Glu Gln Ala | | |
| 500 | 505 | 510 | |
| Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala | Pro Arg Ile Tyr | | |
| 515 | 520 | 525 | |
| Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val | Ile Gly Lys Gly | | |
| 530 | 535 | 540 | |
| Gly Ala Thr Ile Arg Ala Leu Thr Glu Glu | Thr Gly Thr Ser Ile Asp | | |
| 545 | 550 | 555 | 560 |
| Ile Asp Asp Asp Gly Thr Val Lys Ile Ala Ala Val | Asp Gly Asn Ser | | |
| 565 | 570 | 575 | |
| Ala Lys Glu Val Met Ala Arg Ile Glu Asp Ile Thr Ala | Glu Val Glu | | |
| 580 | 585 | 590 | |
| Ala Gly Ala Val Tyr Lys Gly Lys Val Thr Arg Leu | Ala Asp Phe Gly | | |
| 595 | 600 | 605 | |
| Ala Phe Val Ser Ile Val Gly Asn Lys Glu Gly Leu | Val His Ile Ser | | |
| 610 | 615 | 620 | |
| Gln Ile Ala Glu Glu Arg Val Glu Lys Val | Ser Asp Tyr Leu Ala Val | | |
| 625 | 630 | 635 | 640 |
| Gly Gln Glu Val Thr Val Lys Val Val Glu | Ile Asp Arg Gln Gly Arg | | |
| 645 | 650 | 655 | |
| Ile Arg Leu Thr Met Lys Glu Val Ala Pro Lys Gln | Glu His Val Asp | | |
| 660 | 665 | 670 | |
| Ser Val Val Ala Asp Val Ala Ala Glu Glu Asn Ala | | | |
| 675 | 680 | | |

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<220>
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<220>
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<222> (1)...(1512)

<400> 110

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| atg | tgt | ggt | att | gtt | ggt | att | gtt | agc | caa | agc | ccc | gtt | aac | caa | tca | 48 |
| Met | Cys | Gly | Ile | Val | Gly | Ile | Val | Ser | Gln | Ser | Pro | Val | Asn | Gln | Ser | |
| 1 | 5 | | | | | | | 10 | | | | | 15 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| att | tat | gat | gcg | tta | acc | tta | ttg | caa | cac | cgc | ggg | caa | gac | gcc | gcc | 96 |
| Ile | Tyr | Asp | Ala | Leu | Thr | Leu | Leu | Gln | His | Arg | Gly | Gln | Asp | Ala | Ala | |
| 20 | | | | | | | | 25 | | | | | 30 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ggg | att | gta | acc | gta | gat | gat | gaa | aac | cga | ttc | cgc | ttg | cgt | aaa | gcg | 144 |
| Gly | Ile | Val | Thr | Val | Asp | Asp | Glu | Asn | Arg | Phe | Arg | Leu | Arg | Lys | Ala | |
| 35 | | | | | | | 40 | | | | | | 45 | | | |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aac | ggg | tta | gtc | agc | gat | gta | ttt | gaa | caa | gtt | cat | atg | tta | cgt | tta | 192 |
| Asn | Gly | Leu | Val | Ser | Asp | Val | Phe | Glu | Gln | Val | His | Met | Leu | Arg | Leu | |
| 50 | | | | | | | 55 | | | | | 60 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| caa | ggc | aat | gct | ggc | att | gga | cat | gtt | cgt | tat | cct | acg | gct | ggg | agc | 240 |
| Gln | Gly | Asn | Ala | Gly | Ile | Gly | His | Val | Arg | Tyr | Pro | Thr | Ala | Gly | Ser | |
| 65 | | | | | | | 70 | | | 75 | | | 80 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tca | agt | gtc | tct | gaa | gcg | caa | cct | ttt | tat | gta | aat | tcg | cct | tat | ggc | 288 |
| Ser | Ser | Val | Ser | Glu | Ala | Gln | Pro | Phe | Tyr | Val | Asn | Ser | Pro | Tyr | Gly | |
| 85 | | | | | | | 90 | | | | | | 95 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tta | acc | tta | gtg | cat | aat | ggt | aac | ttg | acc | aat | tca | agt | gaa | tta | aaa | 336 |
| Leu | Thr | Leu | Val | His | Asn | Gly | Asn | Leu | Thr | Asn | Ser | Ser | Glu | Leu | Lys | |
| 100 | | | | | | | 105 | | | | | | 110 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gaa | aag | tta | ttt | cgt | ctc | gca | cgt | cgc | cat | gta | aat | acc | aat | tca | gat | 384 |
| Glu | Lys | Leu | Phe | Arg | Leu | Ala | Arg | Arg | His | Val | Asn | Thr | Asn | Ser | Asp | |
| 115 | | | | | | | 120 | | | | | | 125 | | | |

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tct | gaa | tta | tta | ctc | aat | atc | tta | gcc | aat | cac | ctt | gat | cac | ttc | gaa | 432 |
| Ser | Glu | Leu | Leu | Asn | Ile | Leu | Ala | Asn | His | Leu | Asp | His | Phe | Glu | | |
| 130 | | | | | | | 135 | | | | | | 140 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aaa | tac | caa | tta | gat | ccg | caa | gat | gta | ttc | agt | gct | gtc | aaa | caa | acg | 480 |
| Lys | Tyr | Gln | Leu | Asp | Pro | Gln | Asp | Val | Phe | Ser | Ala | Val | Lys | Gln | Thr | |
| 145 | | | | | | | 150 | | | 155 | | | 160 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| cat | cag | gat | att | cgt | ggt | gct | tat | gct | tgt | atc | gcc | atg | att | att | ggt | 528 |
| His | Gln | Asp | Ile | Arg | Gly | Ala | Tyr | Ala | Cys | Ile | Ala | Met | Ile | Ile | Gly | |
| 165 | | | | | | | 170 | | | | | | 175 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| cat | ggt | atg | gtc | gcf | ttt | cgt | gat | ccg | aac | ggt | atc | cgt | ccg | tta | gtg | 576 |
| His | Gly | Met | Val | Ala | Phe | Arg | Asp | Pro | Asn | Gly | Ile | Arg | Pro | Leu | Val | |
| 180 | | | | | | | 185 | | | | | | 190 | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tta | ggg | aaa | cgc | gag | gaa | aat | ggc | aaa | aca | gag | tat | atg | ttt | gcc | tcc | 624 |
| Leu | Gly | Lys | Arg | Glu | Glu | Asn | Gly | Lys | Thr | Glu | Tyr | Met | Phe | Ala | Ser | |

| 195 | 200 | 205 | |
|---|----------------------------|----------------------------|------|
| gaa agt atc gca tta gat aca gtg ggt ttt gag ttt gta cga gat gta
Glu Ser Ile Ala Leu Asp Thr Val Gly Phe Glu Phe Val Arg Asp Val | 210 215 | 220 | 672 |
| caa ccc ggc gaa gcg att tat gtc acg ttt gaa ggg gaa atg tat gct
Gln Pro Gly Glu Ala Ile Tyr Val Thr Phe Glu Gly Glu Met Tyr Ala | 225 230 | 235 240 | 720 |
| cag caa tgc gca gac aaa cca aca tta aca cct tgt att ttt gaa tac
Gln Gln Cys Ala Asp Lys Pro Thr Leu Thr Pro Cys Ile Phe Glu Tyr | 245 | 250 | 768 |
| gtc tat ttt gca cgt cca gac tct tgc atc gat ggg gtt tct gtt tat
Val Tyr Phe Ala Arg Pro Asp Ser Cys Ile Asp Gly Val Ser Val Tyr | 260 | 265 | 816 |
| gct gcc cgt gtt cat atg gga caa cgt tta ggt gaa aaa att gca cgg
Ala Ala Arg Val His Met Gly Gln Arg Leu Gly Glu Lys Ile Ala Arg | 275 | 280 | 864 |
| gaa tgg gcg gat gtg gat gat att gat gtg gtc att cct gtg cct gaa
Glu Trp Ala Asp Val Asp Ile Asp Val Val Ile Pro Val Pro Glu | 290 | 295 | 912 |
| acc tct aac gat att gct tta cgt att gcg cgcc gtg tta aat aaa ccg
Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala Arg Val Leu Asn Lys Pro | 305 | 310 | 960 |
| tat cgt caa ggt ttt gtg aaa aat cgc tat gta gga cgt acg ttt att
Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Gly Arg Thr Phe Ile | 325 | 330 | 1008 |
| atg ccg ggg cag gca ttg cga gtc agt tct gtt aga cgt aaa ctc aat
Met Pro Gly Gln Ala Leu Arg Val Ser Ser Val Arg Arg Lys Leu Asn | 340 | 345 | 1056 |
| acc att gct tca gaa ttt aaa gat aag aat gtg tta tta gtt gac gac
Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn Val Leu Leu Val Asp Asp | 355 | 360 | 1104 |
| tcg att gta cgt ggt acc acg tct gaa caa att gtc gaa atg gcg aga
Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala Arg | 370 | 375 | 1152 |
| gcg gca ggt gcg aag aaa att tat ttt gcc tct gct gca cca gaa att
Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala Ser Ala Ala Pro Glu Ile | 385 | 390 | 1200 |
| cgt tat cca aat gtg tat ggt att gat atg cca acc aaa aat gaa ttg
Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Lys Asn Glu Leu | 405 | 410 | 1248 |
| atc gct tat ggt cgt gat gta gat gaa att gct aac tta att ggt gtg
Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile Ala Asn Leu Ile Gly Val | 420 | 425 | 1296 |
| gat aaa ttg att ttc caa gat ttg gat gcg tta act ggt tct gtg caa
Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala Leu Thr Gly Ser Val Gln | 435 | 440 | 1344 |
| caa gaa aat cca agt att caa gac ttt gat tgt tcg gtg ttt aca ggg | | | 1392 |

| | | | | | | | | | | | | | | | | |
|-----------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| Gln | Glu | Asn | Pro | Ser | Ile | Gln | Asp | Phe | Asp | Cys | Ser | Val | Phe | Thr | Gly | |
| 450 | | | | | | 455 | | | | | | 460 | | | | |
| gtt | tat | gtg | acg | ggc | gat | att | aca | cct | gaa | tat | ctg | gat | aat | att | gca | 1440 |
| Val | Tyr | Val | Thr | Gly | Asp | Ile | Thr | Pro | Glu | Tyr | Leu | Asp | Asn | Ile | Ala | |
| 465 | | | | | 470 | | | | | 475 | | | | 480 | | |
| gaa | cag | cgt | aat | gat | atc | gcc | aag | aaa | aag | cgt | gaa | aaa | gat | gct | acc | 1488 |
| Glu | Gln | Arg | Asn | Asp | Ile | Ala | Lys | Lys | Lys | Arg | Glu | Lys | Asp | Ala | Thr | |
| | | | | | 485 | | | | 490 | | | | 495 | | | |
| aat | ctt | gaa | atg | cac | aat | gaa | aaa | ta | | | | | | | | 1514 |
| Asn | Leu | Glu | Met | His | Asn | Glu | Lys | | | | | | | | | |
| | | | | | 500 | | | | | | | | | | | |
| <210> 111 | | | | | | | | | | | | | | | | |
| <211> 504 | | | | | | | | | | | | | | | | |
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| <400> 111 | | | | | | | | | | | | | | | | |
| Met | Cys | Gly | Ile | Val | Gly | Ile | Val | Ser | Gln | Ser | Pro | Val | Asn | Gln | Ser | |
| 1 | | | | 5 | | | | | 10 | | | | 15 | | | |
| Ile | Tyr | Asp | Ala | Leu | Thr | Leu | Leu | Gln | His | Arg | Gly | Gln | Asp | Ala | Ala | |
| 20 | | | | | 25 | | | | | 30 | | | | | | |
| Gly | Ile | Val | Thr | Val | Asp | Asp | Glu | Asn | Arg | Phe | Arg | Leu | Arg | Lys | Ala | |
| 35 | | | | | 40 | | | | | 45 | | | | | | |
| Asn | Gly | Leu | Val | Ser | Asp | Val | Phe | Glu | Gln | Val | His | Met | Leu | Arg | Leu | |
| 50 | | | | | 55 | | | | | 60 | | | | | | |
| Gln | Gly | Asn | Ala | Gly | Ile | Gly | His | Val | Arg | Tyr | Pro | Thr | Ala | Gly | Ser | |
| 65 | | | | | 70 | | | | 75 | | | | 80 | | | |
| Ser | Ser | Val | Ser | Glu | Ala | Gln | Pro | Phe | Tyr | Val | Asn | Ser | Pro | Tyr | Gly | |
| | | | | 85 | | | | 90 | | | 95 | | | | | |
| Leu | Thr | Leu | Val | His | Asn | Gly | Asn | Leu | Thr | Asn | Ser | Ser | Glu | Leu | Lys | |
| 100 | | | | | 105 | | | | | 110 | | | | | | |
| Glu | Lys | Leu | Phe | Arg | Leu | Ala | Arg | Arg | His | Val | Asn | Thr | Asn | Ser | Asp | |
| 115 | | | | | 120 | | | | | 125 | | | | | | |
| Ser | Glu | Leu | Leu | Leu | Asn | Ile | Leu | Ala | Asn | His | Leu | Asp | His | Phe | Glu | |
| 130 | | | | | 135 | | | | | 140 | | | | | | |
| Lys | Tyr | Gln | Leu | Asp | Pro | Gln | Asp | Val | Phe | Ser | Ala | Val | Lys | Gln | Thr | |
| 145 | | | | | 150 | | | | | 155 | | | 160 | | | |
| His | Gln | Asp | Ile | Arg | Gly | Ala | Tyr | Ala | Cys | Ile | Ala | Met | Ile | Ile | Gly | |
| 165 | | | | | 170 | | | | | 175 | | | | | | |
| His | Gly | Met | Val | Ala | Phe | Arg | Asp | Pro | Asn | Gly | Ile | Arg | Pro | Leu | Val | |
| 180 | | | | | 185 | | | | | 190 | | | | | | |
| Leu | Gly | Lys | Arg | Glu | Glu | Asn | Gly | Lys | Thr | Glu | Tyr | Met | Phe | Ala | Ser | |
| 195 | | | | | 200 | | | | | 205 | | | | | | |
| Glu | Ser | Ile | Ala | Leu | Asp | Thr | Val | Gly | Phe | Glu | Phe | Val | Arg | Asp | Val | |
| 210 | | | | | 215 | | | | | 220 | | | | | | |

Gln Pro Gly Glu Ala Ile Tyr Val Thr Phe Glu Gly Glu Met Tyr Ala
 225 230 235 240
 Gln Gln Cys Ala Asp Lys Pro Thr Leu Thr Pro Cys Ile Phe Glu Tyr
 245 250 255
 Val Tyr Phe Ala Arg Pro Asp Ser Cys Ile Asp Gly Val Ser Val Tyr
 260 265 270 275
 Ala Ala Arg Val His Met Gly Gln Arg Leu Gly Glu Lys Ile Ala Arg
 275 280 285
 Glu Trp Ala Asp Val Asp Asp Ile Asp Val Val Ile Pro Val Pro Glu
 290 295 300
 Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala Arg Val Leu Asn Lys Pro
 305 310 315 320
 Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Gly Arg Thr Phe Ile
 325 330 335
 Met Pro Gly Gln Ala Leu Arg Val Ser Ser Val Arg Arg Lys Leu Asn
 340 345 350
 Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn Val Leu Leu Val Asp Asp
 355 360 365
 Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala Arg
 370 375 380
 Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala Ser Ala Ala Pro Glu Ile
 385 390 395 400
 Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Lys Asn Glu Leu
 405 410 415
 Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile Ala Asn Leu Ile Gly Val
 420 425 430
 Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala Leu Thr Gly Ser Val Gln
 435 440 445
 Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp Cys Ser Val Phe Thr Gly
 450 455 460
 Val Tyr Val Thr Gly Asp Ile Thr Pro Glu Tyr Leu Asp Asn Ile Ala
 465 470 475 480
 Glu Gln Arg Asn Asp Ile Ala Lys Lys Lys Arg Glu Lys Asp Ala Thr
 485 490 495
 Asn Leu Glu Met His Asn Glu Lys
 500

<210> 112
<211> 989
<212> DNA
<213> *Pasteurella multocida*

<220>
<223> rci

<220>
 <221> CDS
 <222> (1)...(987)

| | | | |
|---|--|--|-----|
| <400> 112 | | | |
| atg gca aca ata aga aaa cgt ggt aac tca tat cgt gct gag ata agc | | | 48 |
| Met Ala Thr Ile Arg Lys Arg Gly Asn Ser Tyr Arg Ala Glu Ile Ser | | | |
| 1 5 10 15 | | | |
| aaa aac gga gta agg aaa tca gca aca ttt aag act aaa tca gaa gct | | | 96 |
| Lys Asn Gly Val Arg Lys Ser Ala Thr Phe Thr Lys Ser Glu Ala | | | |
| 20 25 30 | | | |
| aat gcg tgg gct gtt gac gag gag aga aaa tta gct gat ttg gca aaa | | | 144 |
| Asn Ala Trp Ala Val Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys | | | |
| 35 40 45 | | | |
| ggt atc gct cca gat att att ttt aga gat gta ata gaa cgc tat caa | | | 192 |
| Gly Ile Ala Pro Asp Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln | | | |
| 50 55 60 | | | |
| aat gaa gtg tct ata act aaa aaa ggc gcg cga aat gaa att ata aga | | | 240 |
| Asn Glu Val Ser Ile Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg | | | |
| 65 70 75 80 | | | |
| tta aac cgc ttt tta aga tat gat att tct aat ctg tat att cgt gat | | | 288 |
| Leu Asn Arg Phe Leu Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp | | | |
| 85 90 95 | | | |
| tta aga aaa gaa gat ttt gag gag tgg atc aga att cgc cta acc gaa | | | 336 |
| Leu Arg Lys Glu Asp Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu | | | |
| 100 105 110 | | | |
| gta tcg gat gct agc gtt aga cgt gag ctt gtt act ata tcg tca gtg | | | 384 |
| Val Ser Asp Ala Ser Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val | | | |
| 115 120 125 | | | |
| ctg aca aca gca ata aat aag tgg gga tat att tca agg cat cca atg | | | 432 |
| Leu Thr Thr Ala Ile Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met | | | |
| 130 135 140 | | | |
| act ggt att gaa aaa cca aaa aac tcg gca gaa aga aaa gaa cga tat | | | 480 |
| Thr Gly Ile Glu Lys Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr | | | |
| 145 150 155 160 | | | |
| tca gaa cag gac att aaa aca ata tta gaa aca gct aga tat tgt gaa | | | 528 |
| Ser Glu Gln Asp Ile Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu | | | |
| 165 170 175 | | | |
| gat aaa cta ccc ata aca ctc aaa caa aga gta gca att gca atg tta | | | 576 |
| Asp Lys Leu Pro Ile Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu | | | |
| 180 185 190 | | | |
| ttt gct att gaa acc gct atg cgt gct ggt gag att gct agt ata aaa | | | 624 |
| Phe Ala Ile Glu Thr Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys | | | |
| 195 200 205 | | | |
| tgg gat aat gtt ttt ctt gaa aag aga ata gta cat tta ccg aca act | | | 672 |
| Trp Asp Asn Val Phe Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr | | | |
| 210 215 220 | | | |

aaa aac ggg cac tct aga gat gtg ccg ctt tcg caa aga gct gtt gcg 720
 Lys Asn Gly His Ser Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala
 225 230 235 240
 cta att tta aaa atg aaa gag gta gaa aat gga gat ctt gtg ttt cag 768
 Leu Ile Leu Lys Met Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln
 245 250 255
 acc acg cct gaa tca tta agc acc acg ttt aga gtg tta aag aaa gag 816
 Thr Thr Pro Glu Ser Leu Ser Thr Phe Arg Val Leu Lys Lys Glu
 260 265 270
 tgt gga ctt gaa cat ctc cat ttt cat gat acg aga agg gaa gcg ttg 864
 Cys Gly Leu Glu His Leu His Phe His Asp Thr Arg Arg Glu Ala Leu
 275 280 285
 acg aga tta tct aag aaa gta gat gta atg act cta gcc aaa att agc 912
 Thr Arg Leu Ser Lys Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser
 290 295 300
 gga cat aga gat tta aga att tta caa aac aca tat tac gca ccg aat 960
 Gly His Arg Asp Leu Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn
 305 310 315 320
 atg agt gaa gtg gca aac ttg ttg gat ta 989
 Met Ser Glu Val Ala Asn Leu Leu Asp
 325
 <210> 113
 <211> 329
 <212> PRT
 <213> Pasteurella multocida
 <400> 113
 Met Ala Thr Ile Arg Lys Arg Gly Asn Ser Tyr Arg Ala Glu Ile Ser
 1 5 10 15
 Lys Asn Gly Val Arg Lys Ser Ala Thr Phe Lys Thr Lys Ser Glu Ala
 20 25 30
 Asn Ala Trp Ala Val Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys
 35 40 45
 Gly Ile Ala Pro Asp Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln
 50 55 60
 Asn Glu Val Ser Ile Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg
 65 70 75 80
 Leu Asn Arg Phe Leu Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp
 85 90 95
 Leu Arg Lys Glu Asp Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu
 100 105 110
 Val Ser Asp Ala Ser Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val
 115 120 125
 Leu Thr Thr Ala Ile Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met
 130 135 140
 Thr Gly Ile Glu Lys Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 145 | 150 | 155 | 160 | | | | | | | | | | | | |
| Ser | Glu | Gln | Asp | Ile | Lys | Thr | Ile | Leu | Glu | Thr | Ala | Arg | Tyr | Cys | Glu |
| | | | | 165 | | | | 170 | | | | | | 175 | |
| Asp | Lys | Leu | Pro | Ile | Thr | Leu | Lys | Gln | Arg | Val | Ala | Ile | Ala | Met | Leu |
| | | | | 180 | | | 185 | | | | | | 190 | | |
| Phe | Ala | Ile | Glu | Thr | Ala | Met | Arg | Ala | Gly | Glu | Ile | Ala | Ser | Ile | Lys |
| | | | | 195 | | | 200 | | | | | 205 | | | |
| Trp | Asp | Asn | Val | Phe | Leu | Glu | Lys | Arg | Ile | Val | His | Leu | Pro | Thr | Thr |
| | | | | 210 | | 215 | | | | | 220 | | | | |
| Lys | Asn | Gly | His | Ser | Arg | Asp | Val | Pro | Leu | Ser | Gln | Arg | Ala | Val | Ala |
| | | | | 225 | | 230 | | | 235 | | | | 240 | | |
| Leu | Ile | Leu | Lys | Met | Lys | Glu | Val | Glu | Asn | Gly | Asp | Leu | Val | Phe | Gln |
| | | | | 245 | | | 250 | | | | | 255 | | | |
| Thr | Thr | Pro | Glu | Ser | Leu | Ser | Thr | Thr | Phe | Arg | Val | Leu | Lys | Lys | Glu |
| | | | | 260 | | | 265 | | | | | 270 | | | |
| Cys | Gly | Leu | Glu | His | Leu | His | Phe | His | Asp | Thr | Arg | Arg | Glu | Ala | Leu |
| | | | | 275 | | | 280 | | | | 285 | | | | |
| Thr | Arg | Leu | Ser | Lys | Lys | Val | Asp | Val | Met | Thr | Leu | Ala | Lys | Ile | Ser |
| | | | | 290 | | 295 | | | | | 300 | | | | |
| Gly | His | Arg | Asp | Leu | Arg | Ile | Leu | Gln | Asn | Thr | Tyr | Tyr | Ala | Pro | Asn |
| | | | | 305 | | 310 | | | 315 | | | | 320 | | |
| Met | Ser | Glu | Val | Ala | Asn | Leu | Leu | Asp | | | | | | | |
| | | | | | 325 | | | | | | | | | | |

<210> 114
<211> 1190
<212> DNA
<213> Pasteurella multocida

<220>
<223> sopE

<220>
<221> CDS
<222> (1)..(1188)

<400> 114
atg tct gaa gaa tat cta cat ggt gtc aaa gtc aca gaa atc aat caa 48
Met Ser Glu Tyr Leu His Gly Val Lys Val Thr Glu Ile Asn Gln
1 5 10 15

gca att cgc aca att caa agt cta tca acc gca gtc atc ggt att gtc 96
Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly Ile Val
20 25 30

tgt act gca aat gac gca gac aat gaa aca ttc cca ctc aat gaa ccc 144
Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn Glu Pro
35 40 45

gtt ctc atc aca aac gtg gca gcg gca att ggc aag gct gga aaa caa 192
Val Leu Ile Thr Asn Val Ala Ala Ile Gly Lys Ala Gly Gln

| 50 | 55 | 60 | |
|---|----|----|-----|
| ggc acg ctt tca cgt gcg ctt gac ggg att tct gat gta gtc aat tgc
Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val Asn Cys
65 70 75 80 | | | 240 |
| aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac gaa gaa
Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp Glu Glu
85 90 95 | | | 288 |
| aca aaa gca agt gaa atg aac acg gca att att ggc aca atc aca gaa
Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile Thr Glu
100 105 110 | | | 336 |
| gaa ggg cag tac aca ggc ttg aag gcg tta ttg att gcg aaa aac aaa
Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys Asn Lys
115 120 125 | | | 384 |
| ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac aca aaa
Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp Thr Lys
130 135 140 | | | 432 |
| gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac gca ttt
Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Lys Leu Asn Ala Phe
145 150 155 160 | | | 480 |
| gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg gtg caa
Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala Val Gln
165 170 175 | | | 528 |
| tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg ggc gat
Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met Gly Asp
180 185 190 | | | 576 |
| ttt ctg tca ttt aat gtc aac aca tca aaa gtt gag att gac tat gcc
Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala
195 200 205 | | | 624 |
| gtc act cgt gcg gca atg cgt gca tat ctt gat aaa gaa cag ggc
Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly
210 215 220 | | | 672 |
| tgg cat acg tct att tca aat aaa ggc att aat ggc gtg agc ggt gtc
Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val
225 230 235 240 | | | 720 |
| aca caa cca ctc tat ttt gac att aac gac agc tcg act gat gtg aac
Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn
245 250 255 | | | 768 |
| tat ctc aat gaa caa ggc atc acg tgt tgc gtg aat cat aat ggc ttt
Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe
260 265 270 | | | 816 |
| cgt ttt tgg ggc tta cgc acg act gca gaa gat cca tta ttc aag ttt
Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe
275 280 285 | | | 864 |
| gaa gtg tac acc cgc act gca caa atc tta aaa gat acg att gca ggg
Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly
290 295 300 | | | 912 |
| gcg ttt gat tgg gca gtg gat aaa gat att tct gtc acg cta gtg aaa | | | 960 |

Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys
 305 310 315 320
 gat att att gaa gca atc aat gcg aag tgg cgt gat tac acc aca aaa 1008
 Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr Lys
 325 330 335
 ggc tac tta att ggc ggt aaa gcg tgg ctt aat aaa gag ctt aac agt 1056
 Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser
 340 345 350
 gca acg aat tta aaa gat gcg aag ttg ttg atc tct tat gat tat cac 1104
 Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His
 355 360 365
 cca gta cca ccg ctc gaa cag cta ggc ttt aat cag tac att tct gat 1152
 Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp
 370 375 380
 gaa tac ctt gtt gat ttt tca aat cgt tta gca tcg ta 1190
 Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
 385 390 395

 <210> 115
 <211> 396
 <212> PRT
 <213> Pasteurella multocida

 <400> 115
 Met Ser Glu Glu Tyr Leu His Gly Val Lys Val Thr Glu Ile Asn Gln
 1 5 10 15

 Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly Ile Val
 20 25 30

 Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn Glu Pro
 35 40 45

 Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly Lys Gln
 50 55 60

 Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val Asn Cys
 65 70 75 80

 Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp Glu Glu
 85 90 95

 Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile Thr Glu
 100 105 110

 Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys Asn Lys
 115 120 125

 Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp Thr Lys
 130 135 140

 Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn Ala Phe
 145 150 155 160

 Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala Val Gln
 165 170 175

Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met Gly Asp
 180 185 190
 Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala
 195 200 205
 Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly
 210 215 220
 Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val
 225 230 235 240
 Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn
 245 250 255
 Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe
 260 265 270
 Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe
 275 280 285
 Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly
 290 295 300
 Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys
 305 310 315 320
 Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys
 325 330 335
 Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser
 340 345 350
 Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His
 355 360 365
 Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp
 370 375 380
 Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
 385 390 395

<210> 116
 <211> 2204
 <212> DNA
 <213> Pasteurella multocida

<220>
 <223> unkK

<220>
 <221> CDS
 <222> (1)..(2202)

<400> 116
 atg aat aaa aat cgc tat aaa ctc att ttt agt aaa act aaa ggc tgt 48
 Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Lys Thr Lys Gly Cys
 1 5 10 15
 ctt gta cct gtt gct gaa acg att aat tct gca gta gga aat gcc tca 96
 Leu Val Pro Val Ala Glu Thr Ile Asn Ser Ala Val Gly Asn Ala Ser
 20 25 30

| | |
|---|-----|
| tca aaa gac gtt tct gac acc gag ata agt gct tct caa cca gcg ctc
Ser Lys Asp Val Ser Asp Thr Glu Ile Ser Ala Ser Gln Pro Ala Leu
35 40 45 | 144 |
| aac tcg ccg ctt tcg acc ctt tct gta tta gtc aaa acc gca ttt aat
Asn Ser Pro Leu Ser Thr Leu Ser Val Leu Val Lys Thr Ala Phe Asn
50 55 60 | 192 |
| ccg gtt tca aca ttg atg tcg ttg act tgg aaa gaa tac gcc gtt tta
Pro Val Ser Thr Leu Met Ser Leu Thr Trp Lys Glu Tyr Ala Val Leu
65 70 75 80 | 240 |
| tta tta agt gtg gtg tct ttt cct ctt atg gca caa gcc tct gat aca
Leu Leu Ser Val Val Ser Phe Pro Leu Met Ala Gln Ala Ser Asp Thr
85 90 95 | 288 |
| gat tca gtg gta caa aga aaa cct gaa tta act gat gtg acg aat agc
Asp Ser Val Val Gln Arg Lys Pro Glu Leu Thr Asp Val Thr Asn Ser
100 105 110 | 336 |
| aac agc tat cat gtg gaa tta gat aga gag cat cat aaa ggg gag cat
Asn Ser Tyr His Val Glu Leu Asp Arg Glu His His Lys Gly Glu His
115 120 125 | 384 |
| caa aca aaa atc aaa cat act gag aat aat gtc atc att gtt gat att
Gln Thr Lys Ile Lys His Thr Glu Asn Asn Val Ile Ile Val Asp Ile
130 135 140 | 432 |
| gca aaa cca aac caa aag ggc att tca gat aac cgt ttt aaa cac ttc
Ala Lys Pro Asn Gln Lys Gly Ile Ser Asp Asn Arg Phe Lys His Phe
145 150 155 160 | 480 |
| aac atc cca aat ggg gcg gta ttt aac aat agc gcc aag gaa aaa cgc
Asn Ile Pro Asn Gly Ala Val Phe Asn Asn Ser Ala Lys Glu Lys Arg
165 170 175 | 528 |
| tca cag tta gtg ggg tat ttg cca ggt aac cag aat tta acg gaa ggt
Ser Gln Leu Val Gly Tyr Leu Pro Gly Asn Gln Asn Leu Thr Glu Gly
180 185 190 | 576 |
| agt gaa gca aaa gcg atc tta aat cag gtg act gga ccg gat gcc agt
Ser Glu Ala Lys Ala Ile Leu Asn Gln Val Thr Gly Pro Asp Ala Ser
195 200 205 | 624 |
| aaa att gaa ggc gcc ctt gaa att tta ggg caa aaa gcc gat ttg gtg
Lys Ile Glu Gly Ala Leu Glu Ile Leu Gly Gln Lys Ala Asp Leu Val
210 215 220 | 672 |
| att gcg aac caa aat ggc att gtg ctt aat ggg gta aaa acc att aat
Ile Ala Asn Gln Asn Gly Ile Val Leu Asn Gly Val Lys Thr Ile Asn
225 230 235 240 | 720 |
| gcc aat cgt ttt gtg gca aca acc agt agt acc att gat cct gag caa
Ala Asn Arg Phe Val Ala Thr Thr Ser Ser Thr Ile Asp Pro Glu Gln
245 250 255 | 768 |
| atg cag tta aat gtc acg caa ggt aca gtg aca att ggg gtg gat gga
Met Gln Leu Asn Val Thr Gln Gly Thr Val Thr Ile Gly Val Asp Gly
260 265 270 | 816 |
| ttt gcc aca gat ggc tta cct tat ttg gat atc att gcc aaa aag att
Phe Ala Thr Asp Gly Leu Pro Tyr Leu Asp Ile Ile Ala Lys Lys Ile
275 280 285 | 864 |

| | |
|---|------|
| gaa caa aaa caa gcg att aca aaa gaa aga aca gga aat tcc gaa acc
Glu Gln Lys Gln Ala Ile Thr Lys Glu Arg Thr Gly Asn Ser Glu Thr
290 295 300 | 912 |
| gat atc act ttt gtc gca ggt aac agt aaa tat gat tta aag aca cat
Asp Ile Thr Phe Val Ala Gly Asn Ser Lys Tyr Asp Leu Lys Thr His
305 310 315 320 | 960 |
| caa gtg aca gaa aag cat acc gct gag gca caa ggt gaa att gcg att
Gln Val Thr Glu Lys His Thr Ala Glu Ala Gln Gly Glu Ile Ala Ile
325 330 335 | 1008 |
| agc ggt gcg agt acc ggt gca atg tac ggt aaa aat atc aaa tta atc
Ser Gly Ala Ser Thr Gly Ala Met Tyr Gly Lys Asn Ile Lys Leu Ile
340 345 350 | 1056 |
| gta acg gat aaa ggc gct ggg gta aaa cat gat ggc att att tta tct
Val Thr Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser
355 360 365 | 1104 |
| gag gcg gat att caa att gaa acc cat gag ggc gat gtt gaa tta ggc
Glu Ala Asp Ile Gln Ile Glu Thr His Glu Gly Asp Val Glu Leu Gly
370 375 380 | 1152 |
| aat aca aaa aat aat cag aat gag aat tat gcc aaa gct cat gcg gaa
Asn Thr Lys Asn Asn Gln Asn Glu Asn Tyr Ala Lys Ala His Ala Glu
385 390 395 400 | 1200 |
| ggg aat ttt acg gtt aaa ggc ggt aag cac gtt att att ggt aag gaa
Gly Asn Phe Thr Val Lys Gly Lys His Val Ile Ile Gly Lys Glu
405 410 415 | 1248 |
| gtt aaa gcc aac aaa gcg gtc gat att caa gca caa gaa aca aca gta
Val Lys Ala Asn Lys Ala Val Asp Ile Gln Ala Gln Glu Thr Thr Val
420 425 430 | 1296 |
| aga caa aat gcg aaa tta act gcc aaa acg agt gcc aaa att aca gca
Arg Gln Asn Ala Lys Leu Thr Ala Lys Thr Ser Ala Lys Ile Thr Ala
435 440 445 | 1344 |
| agt aag agt gtg aat ctt gaa gat aac gcg aaa ctt att gct aat gag
Ser Lys Ser Val Asn Leu Glu Asp Asn Ala Lys Leu Ile Ala Asn Glu
450 455 460 | 1392 |
| ctg agc aca aca acc aat aaa tta acc aat aaa ggt agc att tac ggc
Leu Ser Thr Thr Asn Lys Leu Thr Asn Lys Gly Ser Ile Tyr Gly
465 470 475 480 | 1440 |
| aag aaa gtg acg cta gat gct gat aat tta gtc aat agt aaa gaa atc
Lys Lys Val Thr Leu Asp Ala Asp Asn Leu Val Asn Ser Lys Glu Ile
485 490 495 | 1488 |
| tat gcg tct agc gaa ctt gat att caa acc aaa ggt cgt gat ctt tta
Tyr Ala Ser Ser Glu Leu Asp Ile Gln Thr Lys Gly Arg Asp Leu Leu
500 505 510 | 1536 |
| ctt gag gat ggg gtt aat caa cca ctg agt ttc tta aaa ggc gct tca
Leu Glu Asp Gly Val Asn Gln Pro Leu Ser Phe Leu Lys Gly Ala Ser
515 520 525 | 1584 |
| ttg tta gcg ccg ggg ttt gtc aac act ggg cta att cac agt aac ggt
Leu Leu Ala Pro Gly Phe Val Asn Thr Gly Leu Ile His Ser Asn Gly
530 535 540 | 1632 |

| | |
|---|------|
| aat gcc aag ctc act ttt aaa gat gac acc agt ttt gtg act gaa gga
Asn Ala Lys Leu Thr Phe Lys Asp Asp Thr Ser Phe Val Thr Glu Gly
545 550 555 560 | 1680 |
| aat aac ttt atc aca gca aaa gac aac tta gaa atc acg gca aaa aat
Asn Asn Phe Ile Thr Ala Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn
565 570 575 | 1728 |
| gtt caa att gat caa gcg aaa aat att caa tta aac gcg aat atc acg
Val Gln Ile Asp Gln Ala Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr
580 585 590 | 1776 |
| atc aat acc aag tct ggt ttt gtg aat tac ggt acc tta gca agt gct
Ile Asn Thr Lys Ser Gly Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala
595 600 605 | 1824 |
| caa aat tta acg att aat acc gaa caa ggc agc att tat aac ata ggc
Gln Asn Leu Thr Ile Asn Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly
610 615 620 | 1872 |
| ggg atc ttg ggg gcg ggt aaa agt ttg aat ctg agc gcg aaa aga gga
Gly Ile Leu Gly Ala Gly Lys Ser Leu Asn Ser Ala Lys Arg Gly
625 630 635 640 | 1920 |
| gaa aac caa gga gga tat ctt att aat caa ggt aag agt cta ctc cat
Glu Asn Gln Gly Gly Tyr Leu Ile Asn Gln Gly Lys Ser Leu Leu His
645 650 655 | 1968 |
| tct gaa ggc gcc atg aac ctc aca gcg gat cgc acg gtg tac aat tta
Ser Glu Gly Ala Met Asn Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu
660 665 670 | 2016 |
| ggg aat att ttt gct aaa ggt gac gcg acg atc aat gca aac gcg tta
Gly Asn Ile Phe Ala Lys Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu
675 680 685 | 2064 |
| att aat gat gtt act ctc aca ggt cgt ctt gag tat caa gat ctg aaa
Ile Asn Asp Val Thr Leu Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys
690 695 700 | 2112 |
| aaa gat tat acg cgt tat tat cgt atc aat gaa acg gca aaa cat ggt
Lys Asp Tyr Thr Arg Tyr Arg Ile Asn Glu Thr Ala Lys His Gly
705 710 715 720 | 2160 |
| tgg cat aat aac ttc tat gaa tta aac gtc gac aga gtt tct tg
Trp His Asn Asn Phe Tyr Glu Leu Asn Val Asp Arg Val Ser
725 730 | 2204 |
|
 | |
| <210> 117 | |
| <211> 734 | |
| <212> PRT | |
| <213> Pasteurella multocida | |
|
 | |
| <400> 117 | |
| Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Lys Thr Lys Gly Cys
1 5 10 15 | |
| Leu Val Pro Val Ala Glu Thr Ile Asn Ser Ala Val Gly Asn Ala Ser
20 25 30 | |
| Ser Lys Asp Val Ser Asp Thr Glu Ile Ser Ala Ser Gln Pro Ala Leu
35 40 45 | |

Asn Ser Pro Leu Ser Thr Leu Ser Val Leu Val Lys Thr Ala Phe Asn
 50 55 60
 Pro Val Ser Thr Leu Met Ser Leu Thr Trp Lys Glu Tyr Ala Val Leu
 65 70 75 80
 Leu Leu Ser Val Val Ser Phe Pro Leu Met Ala Gln Ala Ser Asp Thr
 85 90 95
 Asp Ser Val Val Gln Arg Lys Pro Glu Leu Thr Asp Val Thr Asn Ser
 100 105 110
 Asn Ser Tyr His Val Glu Leu Asp Arg Glu His His Lys Gly Glu His
 115 120 125
 Gln Thr Lys Ile Lys His Thr Glu Asn Asn Val Ile Ile Val Asp Ile
 130 135 140
 Ala Lys Pro Asn Gln Lys Gly Ile Ser Asp Asn Arg Phe Lys His Phe
 145 150 155 160
 Asn Ile Pro Asn Gly Ala Val Phe Asn Asn Ser Ala Lys Glu Lys Arg
 165 170 175
 Ser Gln Leu Val Gly Tyr Leu Pro Gly Asn Gln Asn Leu Thr Glu Gly
 180 185 190
 Ser Glu Ala Lys Ala Ile Leu Asn Gln Val Thr Gly Pro Asp Ala Ser
 195 200 205
 Lys Ile Glu Gly Ala Leu Glu Ile Leu Gly Gln Lys Ala Asp Leu Val
 210 215 220
 Ile Ala Asn Gln Asn Gly Ile Val Leu Asn Gly Val Lys Thr Ile Asn
 225 230 235 240
 Ala Asn Arg Phe Val Ala Thr Thr Ser Ser Thr Ile Asp Pro Glu Gln
 245 250 255
 Met Gln Leu Asn Val Thr Gln Gly Thr Val Thr Ile Gly Val Asp Gly
 260 265 270
 Phe Ala Thr Asp Gly Leu Pro Tyr Leu Asp Ile Ile Ala Lys Lys Ile
 275 280 285
 Glu Gln Lys Gln Ala Ile Thr Lys Glu Arg Thr Gly Asn Ser Glu Thr
 290 295 300
 Asp Ile Thr Phe Val Ala Gly Asn Ser Lys Tyr Asp Leu Lys Thr His
 305 310 315 320
 Gln Val Thr Glu Lys His Thr Ala Glu Ala Gln Gly Glu Ile Ala Ile
 325 330 335
 Ser Gly Ala Ser Thr Gly Ala Met Tyr Gly Lys Asn Ile Lys Leu Ile
 340 345 350
 Val Thr Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser
 355 360 365
 Glu Ala Asp Ile Gln Ile Glu Thr His Glu Gly Asp Val Glu Leu Gly
 370 375 380

Asn Thr Lys Asn Asn Gln Asn Glu Asn Tyr Ala Lys Ala His Ala Glu
 385 390 395 400
 Gly Asn Phe Thr Val Lys Gly Gly Lys His Val Ile Ile Gly Lys Glu
 405 410 415
 Val Lys Ala Asn Lys Ala Val Asp Ile Gln Ala Gln Glu Thr Thr Val
 420 425 430
 Arg Gln Asn Ala Lys Leu Thr Ala Lys Thr Ser Ala Lys Ile Thr Ala
 435 440 445
 Ser Lys Ser Val Asn Leu Glu Asp Asn Ala Lys Leu Ile Ala Asn Glu
 450 455 460
 Leu Ser Thr Thr Thr Asn Lys Leu Thr Asn Lys Gly Ser Ile Tyr Gly
 465 470 475 480
 Lys Lys Val Thr Leu Asp Ala Asp Asn Leu Val Asn Ser Lys Glu Ile
 485 490 495
 Tyr Ala Ser Ser Glu Leu Asp Ile Gln Thr Lys Gly Arg Asp Leu Leu
 500 505 510
 Leu Glu Asp Gly Val Asn Gln Pro Leu Ser Phe Leu Lys Gly Ala Ser
 515 520 525
 Leu Leu Ala Pro Gly Phe Val Asn Thr Gly Leu Ile His Ser Asn Gly
 530 535 540
 Asn Ala Lys Leu Thr Phe Lys Asp Asp Thr Ser Phe Val Thr Glu Gly
 545 550 555 560
 Asn Asn Phe Ile Thr Ala Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn
 565 570 575
 Val Gln Ile Asp Gln Ala Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr
 580 585 590
 Ile Asn Thr Lys Ser Gly Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala
 595 600 605
 Gln Asn Leu Thr Ile Asn Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly
 610 615 620
 Gly Ile Leu Gly Ala Gly Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly
 625 630 635 640
 Glu Asn Gln Gly Gly Tyr Leu Ile Asn Gln Gly Lys Ser Leu Leu His
 645 650 655
 Ser Glu Gly Ala Met Asn Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu
 660 665 670
 Gly Asn Ile Phe Ala Lys Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu
 675 680 685
 Ile Asn Asp Val Thr Leu Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys
 690 695 700
 Lys Asp Tyr Thr Arg Tyr Tyr Arg Ile Asn Glu Thr Ala Lys His Gly
 705 710 715 720

Trp His Asn Asn Phe Tyr Glu Leu Asn Val Asp Arg Val Ser
725 730

<210> 118
<211> 251
<212> DNA
<213> Pasteurella multocida

<220>
<223> unk0

<220>
<221> CDS
<222> (1) .. (249)

<400> 118

atg aaa att act att aca cga aat cat cca gaa gta ttt caa gaa tcc 48
Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser
1 5 10 15

```

gct cgt tta gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca  96
Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
          20           25           30

```

tta aca ttg gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt 144
 Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
 35 40 45

| | |
|---|-----|
| gag gag gaa agc aaa agg gga cat agt att aag gtt gta tta aaa gga | 192 |
| Glu Glu Glu Ser Lys Arg Gly His Ser Ile Lys Val Val Leu Lys Gly | |
| 50 55 60 | |

agt cac gaa gtt att aag tca gag gtg aat aca aat gaa aaa aat cat 240
 Ser His Glu Val Ile Lys Ser Glu Val Asn Thr Asn Glu Lys Asn His
 65 70 75 80

tgt aat cat ta
Cys Asn His 251

<210> 119
<211> 83
<212> PRT
<213> Pasteurella multocida

<400> 119

Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser
 1 5 10 15

Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
20 25 30

Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
35 40 45

Glu .Glu Glu Ser Lys Arg Gly His Ser Ile Lys Val Val Leu Lys Gly
50 55 60

Ser His Glu Val Ile Lys Ser Glu Val Asn Thr Asn Glu Lys Asn His
65 70 75 80

Cys Asn His

<210> 120
<211> 548
<212> DNA
<213> Pasteurella multocida

<220>
<223> unkP

<220>
<221> CDS
<222> (1)..(546)

<400> 120
atg cgt gca tat ctt gat aaa gaa cag ggc tgg cat acg tct att tca 48
Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile Ser
1 5 10 15

aat aaa ggc att aat ggc gtg agc ggt gtc aca caa cca ctc tat ttt 96
Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr Phe
20 25 30

gac att aac gac agc tcg act gat gtg aac tat ctc aat gaa caa ggc 144
Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln Gly
35 40 45

atc acg tgt tgc gtg aat cat aat ggc ttt cgt ttt tgg ggc tta cgc 192
Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu Arg
50 55 60

acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc act 240
Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg Thr
65 70 75 80

gca caa atc tta aaa gat acg att gca ggg gcg ttt gat tgg gca gtg 288
Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala Val
85 90 95

gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca atc 336
Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala Ile
100 105 110

aat gcg aag tgg cgt gat tac acc aca aaa ggc tac tta att ggc ggt 384
Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly Gly
115 120 125

aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa gat 432
Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp
130 135 140

gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc gaa 480
Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu
145 150 155 160

cag cta ggc ttt aat cag tac att tct gat gaa tac ctt gtt gat ttt 528
Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe
165 170 175

tca aat cgt tta gca tcg ta 548

Ser Asn Arg Leu Ala Ser
180

<210> 121
<211> 182
<212> PRT
<213> Pasteurella multocida

<400> 121
Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile Ser
1 5 10 15

Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr Phe
20 25 30

Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln Gly
35 40 45

Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu Arg
50 55 60

Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg Thr
65 70 75 80

Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala Val
85 90 95

Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala Ile
100 105 110

Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly Gly
115 120 125

Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp
130 135 140

Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu
145 150 155 160

Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe
165 170 175

Ser Asn Arg Leu Ala Ser
180

<210> 122
<211> 69
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> apvA-or1

<220>
<221> CDS
<222> (1)...(69)

<400> 122
atg ttt tat gtc atg ctt gcc aat agg acg tct ata att tca tca atc 48
Met Phe Tyr Val Met Leu Ala Asn Arg Thr Ser Ile Ile Ser Ser Ile
1 5 10 15

gat aag ttt aag ata ctt agc
Asp Lys Phe Lys Ile Leu Ser
20

69

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<210> 123
<211> 23
<212> PRT
<213> Actinobacillus pleuropneumoniae

<400> 123
Met Phe Tyr Val Met Leu Ala Asn Arg Thr Ser Ile Ile Ser Ser Ile
      1           5                   10                  15

Asp Lys Phe Lys Ile Leu Ser
      20
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<210> 124
<211> 64
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>
<223> apvA-or2

<220>
<221> CDS
<222> (3) .. (62)

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<400> 124
ag cta agt atc tta aac tta tcg att gat gaa att ata gac gtc cta 47
  Leu Ser Ile Leu Asn Leu Ser Ile Asp Glu Ile Ile Asp Val Leu
    1           5           10          15

```

ttg gca agc atg aca ta 64
Leu Ala Ser Met Thr
20

<210> 125
<211> 20
<212> PRT
<213> *Actinobacillus pleuropneumoniae*

<400> 125
Leu Ser Ile Leu Asn Leu Ser Ile Asp Glu Ile Ile Asp Val Leu Leu
1 5 10 15

Ala Ser Met Thr
20

<210> 126
<211> 653
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>
<223> apvB

<220>
<221> CDS

<222> (1)..(651)

<400> 126
 tta att agc ttt cct ttt att act ttt gca agt aat gtt aat gga gcc 48
 Leu Ile Ser Phe Pro Phe Ile Thr Phe Ala Ser Asn Val Asn Gly Ala
 1 5 10 15
 gaa att gga ttg gga gga gcc cgt gag agt agt att tac tat tct aaa 96
 Glu Ile Gly Leu Gly Gly Ala Arg Glu Ser Ser Ile Tyr Tyr Ser Lys
 20 25 30
 cat aaa gta gca aca aat ccc ttt tta gca ctt gat ctt tct tta ggt 144
 His Lys Val Ala Thr Asn Pro Phe Leu Ala Leu Asp Leu Ser Leu Gly
 35 40 45
 aat ttt tat atg aga ggg act gca gga att agc gaa ata gga tat gaa 192
 Asn Phe Tyr Met Arg Gly Thr Ala Gly Ile Ser Glu Ile Gly Tyr Glu
 50 55 60
 caa tct ttc act gac aat ttc agc gta tca ctg ttt gtt aac cca ttt 240
 Gln Ser Phe Thr Asp Asn Phe Ser Val Ser Leu Phe Val Asn Pro Phe
 65 70 75 80
 gat ggt ttt tca att aaa gga aaa gac ttg tta cct gga tat caa agt 288
 Asp Gly Phe Ser Ile Lys Gly Lys Asp Leu Leu Pro Gly Tyr Gln Ser
 85 90 95
 att caa act cgc aaa act caa ttt gcc ttt ggt tgg gga tta aat tat 336
 Ile Gln Thr Arg Lys Thr Gln Phe Ala Phe Gly Trp Gly Leu Asn Tyr
 100 105 110
 aat ttg gga ggt tta ttc ggc tta aat gat act ttt ata tcc ttg gaa 384
 Asn Leu Gly Gly Leu Phe Gly Leu Asn Asp Thr Phe Ile Ser Leu Glu
 115 120 125
 gga aaa agc gga aaa cgt ggt gcg agt agt aat gtc agc tta ctt aaa 432
 Gly Lys Ser Gly Lys Arg Gly Ala Ser Ser Asn Val Ser Leu Leu Lys
 130 135 140
 tcg ttt aat atg acg aaa aat tgg aaa gtt tca cca tat att ggc tca 480
 Ser Phe Asn Met Thr Lys Asn Trp Lys Val Ser Pro Tyr Ile Gly Ser
 145 150 155 160
 agt tat tat tca tct aaa tat aca gat tat tac ttt ggt att aaa caa 528
 Ser Tyr Tyr Ser Ser Lys Tyr Thr Asp Tyr Tyr Phe Gly Ile Lys Gln
 165 170 175
 tcc gaa tta ggt aat aaa att aca tcc gta tat aaa cct aaa gca gct 576
 Ser Glu Leu Gly Asn Lys Ile Thr Ser Val Tyr Lys Pro Lys Ala Ala
 180 185 190
 tat gca aca cac ata ggt att aat act gat tat gct ttc acg aac aat 624
 Tyr Ala Thr His Ile Gly Ile Asn Thr Asp Tyr Ala Phe Thr Asn Asn
 195 200 205
 ctt ggc atg ggt tta tct gtc ggt tgg at 653
 Leu Gly Met Gly Leu Ser Val Gly Trp
 210 215

<210> 127
<211> 217
<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 127

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Ser | Phe | Pro | Phe | Ile | Thr | Phe | Ala | Ser | Asn | Val | Asn | Gly | Ala |
| 1 | | | | | 5 | | | | 10 | | | | | | 15 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Ile | Gly | Leu | Gly | Gly | Ala | Arg | Glu | Ser | Ser | Ile | Tyr | Tyr | Ser | Lys |
| | | | 20 | | | | 25 | | | | 30 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Lys | Val | Ala | Thr | Asn | Pro | Phe | Leu | Ala | Leu | Asp | Leu | Ser | Leu | Gly |
| | | | 35 | | | | 40 | | | 45 | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Phe | Tyr | Met | Arg | Gly | Thr | Ala | Gly | Ile | Ser | Glu | Ile | Gly | Tyr | Glu |
| | | | 50 | | | 55 | | | 60 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gln | Ser | Phe | Thr | Asp | Asn | Phe | Ser | Val | Ser | Leu | Phe | Val | Asn | Pro | Phe |
| | | | 65 | | | 70 | | | 75 | | | 80 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Gly | Phe | Ser | Ile | Lys | Gly | Lys | Asp | Leu | Leu | Pro | Gly | Tyr | Gln | Ser |
| | | | 85 | | | 90 | | | 95 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Gln | Thr | Arg | Lys | Thr | Gln | Phe | Ala | Phe | Gly | Trp | Gly | Leu | Asn | Tyr |
| | | | 100 | | | 105 | | | 110 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Leu | Gly | Gly | Leu | Phe | Gly | Leu | Asn | Asp | Thr | Phe | Ile | Ser | Leu | Glu |
| | | | 115 | | | 120 | | | 125 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Lys | Ser | Gly | Lys | Arg | Gly | Ala | Ser | Ser | Asn | Val | Ser | Leu | Leu | Lys |
| | | | 130 | | | 135 | | | 140 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Phe | Asn | Met | Thr | Lys | Asn | Trp | Lys | Val | Ser | Pro | Tyr | Ile | Gly | Ser |
| | | | 145 | | | 150 | | | 155 | | | 160 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Tyr | Tyr | Ser | Ser | Lys | Tyr | Thr | Asp | Tyr | Tyr | Phe | Gly | Ile | Lys | Gln |
| | | | 165 | | | 170 | | | 175 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Glu | Leu | Gly | Asn | Lys | Ile | Thr | Ser | Val | Tyr | Lys | Pro | Lys | Ala | Ala |
| | | | 180 | | | 185 | | | 190 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Ala | Thr | His | Ile | Gly | Ile | Asn | Thr | Asp | Tyr | Ala | Phe | Thr | Asn | Asn |
| | | | 195 | | | 200 | | | 205 | | | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|--|
| Leu | Gly | Met | Gly | Leu | Ser | Val | Gly | Trp | | | | | | | |
| | | | 210 | | | 215 | | | | | | | | | |

<210> 128

<211> 242

<212> DNA

<213> *Actinobacillus pleuropneumoniae*

<220>

<223> apvC

<220>

<221> CDS

<222> (1)..(240)

<400> 128

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| atg | tgg | cgg | atg | gga | gat | ttt | atg | tct | aaa | aaa | gag | agg | ctg | aat | gat | 48 |
| Met | Trp | Arg | Met | Gly | Asp | Phe | Met | Ser | Lys | Lys | Glu | Arg | Leu | Asn | Asp | |
| 1 | | | | | 5 | | | | 10 | | | | 15 | | | |

| | | | |
|---|-----|----|-----|
| atg gct cgc cag att tta tca gcg gcg gag ttg ctc att gca aag gaa | 96 | | |
| Met Ala Arg Gln Ile Leu Ser Ala Ala Glu Leu Leu Ile Ala Lys Glu | | | |
| 20 | 25 | 30 | |
| ggt ttg caa aat tta tcg atg agg aaa atc gca agt gaa gcc ggt atc | 144 | | |
| Gly Leu Gln Asn Leu Ser Met Arg Lys Ile Ala Ser Glu Ala Gly Ile | | | |
| 35 | 40 | 45 | |
| gca aca ggc acg ctt tat ctc tat ttc aaa acg aaa gac gag tta ctg | 192 | | |
| Ala Thr Gly Thr Leu Tyr Leu Tyr Phe Lys Thr Lys Asp Glu Leu Leu | | | |
| 50 | 55 | 60 | |
| gat tgt ttg gcg gaa caa tta cat gaa cga tat tat cgt tat ctg aat | 240 | | |
| Asp Cys Leu Ala Glu Gln Leu His Glu Arg Tyr Tyr Arg Tyr Leu Asn | | | |
| 65 | 70 | 75 | 80 |
| at | | | 242 |
|
 | | | |
| <210> 129 | | | |
| <211> 80 | | | |
| <212> PRT | | | |
| <213> Actinobacillus pleuropneumoniae | | | |
|
 | | | |
| <400> 129 | | | |
| Met Trp Arg Met Gly Asp Phe Met Ser Lys Lys Glu Arg Leu Asn Asp | | | |
| 1 | 5 | 10 | 15 |
| Met Ala Arg Gln Ile Leu Ser Ala Ala Glu Leu Leu Ile Ala Lys Glu | | | |
| 20 | 25 | 30 | |
| Gly Leu Gln Asn Leu Ser Met Arg Lys Ile Ala Ser Glu Ala Gly Ile | | | |
| 35 | 40 | 45 | |
| Ala Thr Gly Thr Leu Tyr Leu Tyr Phe Lys Thr Lys Asp Glu Leu Leu | | | |
| 50 | 55 | 60 | |
| Asp Cys Leu Ala Glu Gln Leu His Glu Arg Tyr Tyr Arg Tyr Leu Asn | | | |
| 65 | 70 | 75 | 80 |
|
 | | | |
| <210> 130 | | | |
| <211> 527 | | | |
| <212> DNA | | | |
| <213> Actinobacillus pleuropneumoniae | | | |
|
 | | | |
| <220> | | | |
| <223> apvD | | | |
|
 | | | |
| <220> | | | |
| <221> CDS | | | |
| <222> (1)...(525) | | | |
|
 | | | |
| <400> 130 | | | |
| aat att caa aaa aca gtt att gct agc ggc aca ttg caa gcg act gaa | 48 | | |
| Asn Ile Gln Lys Thr Val Ile Ala Ser Gly Thr Leu Gln Ala Thr Glu | | | |
| 1 | 5 | 10 | 15 |
| caa gta gat att ggt gca caa gta tct ggg cag att aag cat att tta | 96 | | |
| Gln Val Asp Ile Gly Ala Gln Val Ser Gly Gln Ile Lys His Ile Leu | | | |
| 20 | 25 | 30 | |
| gta caa gaa gga cag aag gtt aaa aaa ggt gag cta tta gct gta att | 144 | | |

| | | | |
|---|-----|-----|-----|
| Val Gln Glu Gly Gln Lys Val Lys Lys Gly Glu Leu Leu Ala Val Ile | | | |
| 35 | 40 | 45 | |
| gat cca cgt ctg gct gaa acg gaa tta aaa cta gca aaa gct gag cta | | | 192 |
| Asp Pro Arg Leu Ala Glu Thr Glu Leu Lys Leu Ala Lys Ala Glu Leu | | | |
| 50 | 55 | 60 | |
| gca aat gct tct gct aat ttg gat aca aaa aaa att aat ctt aag caa | | | 240 |
| Ala Asn Ala Ser Ala Asn Leu Asp Thr Lys Lys Ile Asn Leu Lys Gln | | | |
| 65 | 70 | 75 | 80 |
| ctg caa tca gat tgg gaa cgt cat caa cgt ttg ata cga acc aat gcg | | | 288 |
| Leu Gln Ser Asp Trp Glu Arg His Gln Arg Leu Ile Arg Thr Asn Ala | | | |
| 85 | 90 | 95 | |
| aca agc caa aag gaa aca gaa gca aaa agt aga tta aat acg gcc | | | 336 |
| Thr Ser Gln Lys Glu Thr Glu Ala Lys Ser Arg Leu Asn Thr Ala | | | |
| 100 | 105 | 110 | |
| aaa gca gaa ctt caa att gcg caa aat aat cta gat atc gct aaa atc | | | 384 |
| Lys Ala Glu Leu Gln Ile Ala Gln Asn Asn Leu Asp Ile Ala Lys Ile | | | |
| 115 | 120 | 125 | |
| aga gtg gaa aaa gct gaa acc gaa cta gga tat aca gaa att cgt tct | | | 432 |
| Arg Val Glu Lys Ala Glu Thr Glu Leu Gly Tyr Thr Glu Ile Arg Ser | | | |
| 130 | 135 | 140 | |
| cca ctt gat gca aca gta att tca gta ttt gcg caa aat ggt caa act | | | 480 |
| Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr | | | |
| 145 | 150 | 155 | 160 |
| tta gtc acc acc caa caa gta cca gtg ctg atg aaa tta gct aat at | | | 527 |
| Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn | | | |
| 165 | 170 | 175 | |

<210> 131

<211> 175

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 131

| | | | |
|---|---|----|----|
| Asn Ile Gln Lys Thr Val Ile Ala Ser Gly Thr Leu Gln Ala Thr Glu | | | |
| 1 | 5 | 10 | 15 |

| | | | |
|---|----|----|--|
| Gln Val Asp Ile Gly Ala Gln Val Ser Gly Gln Ile Lys His Ile Leu | | | |
| 20 | 25 | 30 | |

| | | | |
|---|----|----|--|
| Val Gln Glu Gly Gln Lys Val Lys Lys Gly Glu Leu Leu Ala Val Ile | | | |
| 35 | 40 | 45 | |

| | | | |
|---|----|----|--|
| Asp Pro Arg Leu Ala Glu Thr Glu Leu Lys Leu Ala Lys Ala Glu Leu | | | |
| 50 | 55 | 60 | |

| | | | |
|---|----|----|----|
| Ala Asn Ala Ser Ala Asn Leu Asp Thr Lys Lys Ile Asn Leu Lys Gln | | | |
| 65 | 70 | 75 | 80 |

| | | | |
|---|----|----|--|
| Leu Gln Ser Asp Trp Glu Arg His Gln Arg Leu Ile Arg Thr Asn Ala | | | |
| 85 | 90 | 95 | |

| | | | |
|---|-----|-----|--|
| Thr Ser Gln Lys Glu Thr Glu Ala Lys Ser Arg Leu Asn Thr Ala | | | |
| 100 | 105 | 110 | |

Lys Ala Glu Leu Gln Ile Ala Gln Asn Asn Leu Asp Ile Ala Lys Ile
 115 120 125

Arg Val Glu Lys Ala Glu Thr Glu Leu Gly Tyr Thr Glu Ile Arg Ser
 130 135 140

Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr
 145 150 155 160

Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn
 165 170 175

<210> 132

<211> 867

<212> DNA

<213> *Actinobacillus pleuropneumoniae*

<220>

<223> atpG

<220>

<221> CDS

<222> (1)...(864)

<400> 132

| | |
|---|----|
| atg gca ggt gcg aaa gag ata aga acc aaa att gca agt gtg aaa aat | 48 |
| Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys Asn | |
| 1 5 10 15 | |

| | |
|---|----|
| act caa aaa atc acc aaa gca atg gaa atg gtt gct acc tct aaa atg | 96 |
| Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Thr Ser Lys Met | |
| 20 25 30 | |

| | |
|---|-----|
| cgt aaa acg caa gag cgt atg gct gcc agt cgt cct tat tcg gaa aca | 144 |
| Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ser Glu Thr | |
| 35 40 45 | |

| | |
|---|-----|
| atc cgt aag gtg att agc cat att gcg aaa gga agc att ggt tat aag | 192 |
| Ile Arg Lys Val Ile Ser His Ile Ala Lys Gly Ser Ile Gly Tyr Lys | |
| 50 55 60 | |

| | |
|---|-----|
| cac ccg ttt tta act gaa cgt gat att aaa aaa gta ggc tat ctt gtc | 240 |
| His Pro Phe Leu Thr Glu Arg Asp Ile Lys Lys Val Gly Tyr Leu Val | |
| 65 70 75 80 | |

| | |
|---|-----|
| gtt tcg acc gat cgc ggt tta tgc ggt ggc ctt aat atc aat tta ttc | 288 |
| Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe | |
| 85 90 95 | |

| | |
|---|-----|
| aaa gcg act ttg aat gaa ttt aaa acg tgg aaa gat aaa gac gtt agt | 336 |
| Lys Ala Thr Leu Asn Glu Phe Lys Thr Trp Lys Asp Lys Asp Val Ser | |
| 100 105 110 | |

| | |
|---|-----|
| gtt gag ctt ggt tta gta ggg tcg aaa ggc gta agc ttt tac caa aat | 384 |
| Val Glu Leu Gly Leu Val Gly Ser Lys Gly Val Ser Phe Tyr Gln Asn | |
| 115 120 125 | |

| | |
|---|-----|
| cta ggc tta aac gtg aga tct caa gta acg gga tta ggc gat aat ccg | 432 |
| Leu Gly Leu Asn Val Arg Ser Gln Val Thr Gly Leu Gly Asp Asn Pro | |
| 130 135 140 | |

gaa atg gaa cgt atc gtg ggc gca gtt aat gaa atg att aat gcg ttc 480

| | | | |
|---|-----|-----|-----|
| Glu Met Glu Arg Ile Val Gly Ala Val Asn Glu Met Ile Asn Ala Phe | | | |
| 145 | 150 | 155 | 160 |
| cga aac gga gaa gtg gat gcg gtt tac gtc gct tac aac cgt ttt gaa | | | 528 |
| Arg Asn Gly Glu Val Asp Ala Val Tyr Val Ala Tyr Asn Arg Phe Glu | | | |
| 165 | 170 | 175 | |
| aat acg atg tca caa aaa cct gtt atc gca cag tta ctt ccg tta cct | | | 576 |
| Asn Thr Met Ser Gln Lys Pro Val Ile Ala Gln Leu Leu Pro Leu Pro | | | |
| 180 | 185 | 190 | |
| aaa cta gat gac gat gaa tta gat acg aaa ggt tca tgg gat tat att | | | 624 |
| Lys Leu Asp Asp Asp Glu Leu Asp Thr Lys Gly Ser Trp Asp Tyr Ile | | | |
| 195 | 200 | 205 | |
| tat gaa ccg aat cca caa gtt tta ttg gat agt tta ctt gtt cgt tat | | | 672 |
| Tyr Glu Pro Asn Pro Gln Val Leu Leu Asp Ser Leu Leu Val Arg Tyr | | | |
| 210 | 215 | 220 | |
| tta gaa act cag gta tac caa gca gtt gta gat aac cta gct tct gaa | | | 720 |
| Leu Glu Thr Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu | | | |
| 225 | 230 | 235 | 240 |
| caa gcc gct cga atg gta gcg atg aaa gcc gca aca gat aat gcg ggt | | | 768 |
| Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly | | | |
| 245 | 250 | 255 | |
| aca tta atc gat gaa tta caa tta gtg tat aac aaa gct cgc caa gca | | | 816 |
| Thr Leu Ile Asp Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala | | | |
| 260 | 265 | 270 | |
| agc att aca aat gaa tta aac gaa att gtt gcg ggt gcc gca gca att | | | 864 |
| Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile | | | |
| 275 | 280 | 285 | |
| taa | | | 867 |
| <210> 133 | | | |
| <211> 288 | | | |
| <212> PRT | | | |
| <213> Actinobacillus pleuropneumoniae | | | |
| <400> 133 | | | |
| Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys Asn | | | |
| 1 5 10 15 | | | |
| Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Thr Ser Lys Met | | | |
| 20 25 30 | | | |
| Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ser Glu Thr | | | |
| 35 40 45 | | | |
| Ile Arg Lys Val Ile Ser His Ile Ala Lys Gly Ser Ile Gly Tyr Lys | | | |
| 50 55 60 | | | |
| His Pro Phe Leu Thr Glu Arg Asp Ile Lys Lys Val Gly Tyr Leu Val | | | |
| 65 70 75 80 | | | |
| Val Ser Thr Asp Arg Gly Leu Cys Gly Leu Asn Ile Asn Leu Phe | | | |
| 85 90 95 | | | |

Lys Ala Thr Leu Asn Glu Phe Lys Thr Trp Lys Asp Lys Asp Val Ser
 100 105 110
 Val Glu Leu Gly Leu Val Gly Ser Lys Gly Val Ser Phe Tyr Gln Asn
 115 120 125
 Leu Gly Leu Asn Val Arg Ser Gln Val Thr Gly Leu Gly Asp Asn Pro
 130 135 140
 Glu Met Glu Arg Ile Val Gly Ala Val Asn Glu Met Ile Asn Ala Phe
 145 150 155 160
 Arg Asn Gly Glu Val Asp Ala Val Tyr Val Ala Tyr Asn Arg Phe Glu
 165 170 175
 Asn Thr Met Ser Gln Lys Pro Val Ile Ala Gln Leu Leu Pro Leu Pro
 180 185 190
 Lys Leu Asp Asp Asp Glu Leu Asp Thr Lys Gly Ser Trp Asp Tyr Ile
 195 200 205
 Tyr Glu Pro Asn Pro Gln Val Leu Leu Asp Ser Leu Leu Val Arg Tyr
 210 215 220
 Leu Glu Thr Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu
 225 230 235 240
 Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly
 245 250 255
 Thr Leu Ile Asp Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala
 260 265 270
 Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile
 275 280 285

<210> 134

<211> 534

<212> DNA

<213> *Actinobacillus pleuropneumoniae*

<220>

<223> atpH

<220>

<221> CDS

<222> (1)...(531)

<400> 134

| | |
|---|----|
| atg tca gaa tta agt aca gta gct cgc ccc tac gct aaa gca gct ttt | 48 |
| Met Ser Glu Leu Ser Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe | |
| 1 5 10 15 | |

| | |
|---|----|
| gat ttt gct tta gaa caa ggt cag ttg gac aaa tgg caa gaa atg tta | 96 |
| Asp Phe Ala Leu Glu Gln Gly Gln Leu Asp Lys Trp Gln Glu Met Leu | |
| 20 25 30 | |

| | |
|---|-----|
| cag ttt tcg gca ttc gtt gct gaa aac gaa caa gtg gcg gaa tat att | 144 |
| Gln Phe Ser Ala Phe Val Ala Glu Asn Glu Gln Val Ala Glu Tyr Ile | |
| 35 40 45 | |

| | |
|---|-----|
| aat tct tcc ctt gca agc ggt cag att tct gaa act ttt atc aaa atc | 192 |
|---|-----|

| | | | |
|---|-----|-----|-----|
| Asn Ser Ser Leu Ala Ser Gly Gln Ile Ser Glu Thr Phe Ile Lys Ile | | | |
| 50 | 55 | 60 | |
| tgc ggc gac caa ctt gat caa tat ggg caa aat ttt att cgt gta atg | | | 240 |
| Cys Gly Asp Gln Leu Asp Gln Tyr Gly Gln Asn Phe Ile Arg Val Met | | | |
| 65 | 70 | 75 | 80 |
| gct gaa aat aaa cgt ctg gct gtg ttg cct atg gtt ttt gat act ttc | | | 288 |
| Ala Glu Asn Lys Arg Leu Ala Val Leu Pro Met Val Phe Asp Thr Phe | | | |
| 85 | 90 | 95 | |
| gta tca tta cga gcg gaa cat gaa gcg gta aaa gat gta aca att gtt | | | 336 |
| Val Ser Leu Arg Ala Glu His Glu Ala Val Lys Asp Val Thr Ile Val | | | |
| 100 | 105 | 110 | |
| tcg gca aac gaa tta agt caa gca caa gaa gat aaa atc gca aaa gcg | | | 384 |
| Ser Ala Asn Glu Leu Ser Gln Ala Gln Glu Asp Lys Ile Ala Lys Ala | | | |
| 115 | 120 | 125 | |
| atg gaa aaa cgc tta ggt caa aaa gtt cgt tta acc aac caa atc gat | | | 432 |
| Met Glu Lys Arg Leu Gly Gln Lys Val Arg Leu Thr Asn Gln Ile Asp | | | |
| 130 | 135 | 140 | |
| aac agc ctg att gca ggc gta att att aaa tac gat gat gtt gtt att | | | 480 |
| Asn Ser Leu Ile Ala Gly Val Ile Lys Tyr Asp Asp Val Val Ile | | | |
| 145 | 150 | 155 | 160 |
| gat ggt agt agc cgc ggt cag tta aat cgc tta gcg tca gcg ttg agc | | | 528 |
| Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser | | | |
| 165 | 170 | 175 | |
| ttg taa | | | 534 |
| Leu | | | |
| <210> 135 | | | |
| <211> 177 | | | |
| <212> PRT | | | |
| <213> <i>Actinobacillus pleuropneumoniae</i> | | | |
| <400> 135 | | | |
| Met Ser Glu Leu Ser Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe | | | |
| 1 | 5 | 10 | 15 |
| Asp Phe Ala Leu Glu Gln Gly Gln Leu Asp Lys Trp Gln Glu Met Leu | | | |
| 20 | 25 | 30 | |
| Gln Phe Ser Ala Phe Val Ala Glu Asn Glu Gln Val Ala Glu Tyr Ile | | | |
| 35 | 40 | 45 | |
| Asn Ser Ser Leu Ala Ser Gly Gln Ile Ser Glu Thr Phe Ile Lys Ile | | | |
| 50 | 55 | 60 | |
| Cys Gly Asp Gln Leu Asp Gln Tyr Gly Gln Asn Phe Ile Arg Val Met | | | |
| 65 | 70 | 75 | 80 |
| Ala Glu Asn Lys Arg Leu Ala Val Leu Pro Met Val Phe Asp Thr Phe | | | |
| 85 | 90 | 95 | |
| Val Ser Leu Arg Ala Glu His Glu Ala Val Lys Asp Val Thr Ile Val | | | |
| 100 | 105 | 110 | |

Ser Ala Asn Glu Leu Ser Gln Ala Gln Glu Asp Lys Ile Ala Lys Ala
 115 120 125

Met Glu Lys Arg Leu Gly Gln Lys Val Arg Leu Thr Asn Gln Ile Asp
 130 135 140

Asn Ser Leu Ile Ala Gly Val Ile Ile Lys Tyr Asp Asp Val Val Ile
 145 150 155 160

Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser
 165 170 175

Leu

<210> 136

<211> 321

<212> DNA

<213> *Actinobacillus pleuropneumoniae*

<220>

<223> dksA

<220>

<221> CDS

<222> (1)..(318)

<400> 136

| | |
|---|----|
| gca tgg cat gtg caa att atg gac gaa gct gag cgt aca aaa aac caa | 48 |
| Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln | |
| 1 5 10 15 | |

| | |
|---|----|
| atg cag gaa gaa gtc gct aat ttc gcc gat cct gcg gac cgc gcc act | 96 |
| Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr | |
| 20 25 30 | |

| | |
|---|-----|
| cag gaa gaa gaa ttc agt ctt gaa tta aga aac cgt gac cgt gag cgt | 144 |
| Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Asp Arg Glu Arg | |
| 35 40 45 | |

| | |
|---|-----|
| aaa ttg ctt aag aag att gag caa acg tta aat agc att gcc gaa gac | 192 |
| Lys Leu Leu Lys Lys Ile Glu Gln Thr Leu Asn Ser Ile Ala Glu Asp | |
| 50 55 60 | |

| | |
|---|-----|
| gaa tac ggc tat tgc gaa act tgc ggt gtt gaa atc ggt tta cgt cgt | 240 |
| Glu Tyr Gly Tyr Cys Glu Thr Cys Gly Val Glu Ile Gly Leu Arg Arg | |
| 65 70 75 80 | |

| | |
|---|-----|
| tta gaa gcg cgc ccg acc gcg gat atg tgt atc gat tgc aaa aca ctt | 288 |
| Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu | |
| 85 90 95 | |

| | |
|---|-----|
| gcg gaa atc cgt gaa aag caa atg ggc tta taa | 321 |
| Ala Glu Ile Arg Glu Lys Gln Met Gly Leu | |
| 100 105 | |

<210> 137

<211> 106

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 137
 Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln
 1 5 10 15
 Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr
 20 25 30
 Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Asp Arg Glu Arg
 35 40 45
 Lys Leu Leu Lys Lys Ile Glu Gln Thr Leu Asn Ser Ile Ala Glu Asp
 50 55 60
 Glu Tyr Gly Tyr Cys Glu Thr Cys Gly Val Glu Ile Gly Leu Arg Arg
 65 70 75 80
 Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu
 85 90 95
 Ala Glu Ile Arg Glu Lys Gln Met Gly Leu
 100 105

<210> 138
<211> 33
<212> DNA
<213> *Actinobacillus pleuropneumoniae*
<220>
<223> dnaK
<220>
<221> CDS
<222> (1)..(30)
<400> 138
gct gag ttt gaa gaa gtg aaa gat aat aaa taa 33
Ala Glu Phe Glu Glu Val Lys Asp Asn Lys
1 5 10

<210> 139
<211> 10
<212> PRT
<213> *Actinobacillus pleuropneumoniae*
<400> 139
Ala Glu Phe Glu Glu Val Lys Asp Asn Lys
1 5 10

<210> 140
<211> 453
<212> DNA
<213> *Actinobacillus pleuropneumoniae*
<220>
<223> exbB
<220>
<221> CDS
<222> (1)..(450)

<400> 140
atg gaa caa atg ctt gaa ctt tta caa ggt cat gtt gat tat att att 48
Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile
1 5 10 15

tta ggc tta tta cta tta atg agt gtt gtg ttg gta tgg aaa att att 96
Leu Gly Leu Leu Leu Met Ser Val Val Leu Val Trp Lys Ile Ile
20 25 30

gaa cgc gta ctt ttc tac aaa caa ttg gat gtg acc aaa tat gac acg 144
Glu Arg Val Leu Phe Tyr Lys Gln Leu Asp Val Thr Lys Tyr Asp Thr
35 40 45

cta caa gat ttg gaa att gat acc act cgc aat tta acc acc att tcc 192
Leu Gln Asp Leu Glu Ile Asp Thr Thr Arg Asn Leu Thr Thr Ile Ser
50 55 60

act atc ggt gcc aac gcc cct tat atc ggt tta tta gga acc gta tta 240
Thr Ile Gly Ala Asn Ala Pro Tyr Ile Gly Leu Leu Gly Thr Val Leu
65 70 75 80

ggg atc tta ctt acc ttc tat cat tta ggg cat tcc ggc ggt gat att 288
Gly Ile Leu Leu Thr Phe Tyr His Leu Gly His Ser Gly Gly Asp Ile
85 90 95

gac gcc gca tcc att atg gtt cac ctt tcg ctt gca tta aaa gca acc 336
Asp Ala Ala Ser Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr
100 105 110

gca gcc ggt atc tta gtc gct att ccg gca atg atg ttc tac agc ggt 384
Ala Ala Gly Ile Leu Val Ala Ile Pro Ala Met Met Phe Tyr Ser Gly
115 120 125

ttt aac cgt aaa gtg gat gaa agc aaa ctt aaa tgg caa gcg att caa 432
Phe Asn Arg Lys Val Asp Glu Ser Lys Leu Lys Trp Gln Ala Ile Gln
130 135 140

gct cgt aaa gcc aat caa taa 453
Ala Arg Lys Ala Asn Gln
145 150

<210> 141
<211> 150
<212> PRT
<213> *Actinobacillus pleuropneumoniae*

<400> 141
Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile 15
1 5 10 15

Leu Gly Leu Leu Leu Met Ser Val Val Leu Val Trp Lys Ile Ile
20 25 30

Glu Arg Val Leu Phe Tyr Lys Gln Leu Asp Val Thr Lys Tyr Asp Thr
35 40 45

Leu Gln Asp Leu Glu Ile Asp Thr Thr Arg Asn Leu Thr Thr Ile Ser
50 55 60

Thr Ile Gly Ala Asn Ala Pro Tyr Ile Gly Leu Leu Gly Thr Val Leu
65 70 75 80

Gly Ile Leu Leu Thr Phe Tyr His Leu Gly His Ser Gly Gly Asp Ile
85 90 95

Asp Ala Ala Ser Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr
100 105 110

Ala Ala Gly Ile Leu Val Ala Ile Pro Ala Met Met Phe Tyr Ser Gly
115 120 125

Phe Asn Arg Lys Val Asp Glu Ser Lys Leu Lys Trp Gln Ala Ile Gln
130 135 140

Ala Arg Lys Ala Asn Gln
145 150

<210> 142

<211> 720

<212> DNA

<213> *Actinobacillus pleuropneumoniae*

<220>

<223> fkpA

<220>

<221> CDS

<222> (1)..(717)

<400> 142

atg tta aaa aat aaa ctt tct gtt ctt gca atc gta gcc ggt acg ttc 48
Met Leu Lys Asn Lys Leu Ser Val Leu Ala Ile Val Ala Gly Thr Phe
1 5 10 15

gtt tca gct caa act gca ttt gca gcg gat caa aaa ttc att gac gat 96
Val Ser Ala Gln Thr Ala Phe Ala Ala Asp Gln Lys Phe Ile Asp Asp
20 25 30

tca tca tat gca gtc ggc gta ttg atg ggt aaa aat atc gaa ggc gtc 144
Ser Ser Tyr Ala Val Gly Val Leu Met Gly Lys Asn Ile Glu Gly Val
35 40 45

gtt gaa tca caa aaa gaa att ttt tct tat aac caa gat aaa atc ttg 192
Val Glu Ser Gln Lys Glu Ile Phe Ser Tyr Asn Gln Asp Lys Ile Leu
50 55 60

gcg ggt gtc caa gat acc atc aaa aaa acc ggt aaa tta acc gat gaa 240
Ala Gly Val Gln Asp Thr Ile Lys Lys Thr Gly Lys Leu Thr Asp Glu
65 70 75 80

gat cta caa aaa caa tta aaa tcg ctt gat act tat ctt gca agt caa 288
Asp Leu Gln Lys Gln Leu Lys Ser Leu Asp Thr Tyr Leu Ala Ser Gln
85 90 95

gaa agc aaa att gcg gcg gag aaa agc aaa gca acc gta gaa gcc ggt 336
Glu Ser Lys Ile Ala Ala Glu Lys Ser Lys Ala Thr Val Glu Ala Gly
100 105 110

aat aaa ttt cgt acc gac tac gaa aaa caa agc ggc gtg aaa aaa acc 384
Asn Lys Phe Arg Thr Asp Tyr Glu Lys Gln Ser Gly Val Lys Lys Thr
115 120 125

gct tcc ggt tta ctt tat aaa att gaa aaa gcc ggc acg ggc gaa tcg 432

| | | | |
|---|-----|-----|-----|
| Ala Ser Gly Leu Leu Tyr Lys Ile Glu Lys Ala Gly Thr Gly Glu Ser | | | |
| 130 | 135 | 140 | |
| cct aaa gcg gaa gat acc gtt aaa gtt cac tat aaa ggg aca tta acc | 480 | | |
| Pro Lys Ala Glu Asp Thr Val Lys Val His Tyr Lys Gly Thr Leu Thr | | | |
| 145 | 150 | 155 | 160 |
| gat ggt acg gta ttc gat agc tca tac gat cgc ggt gag ccg att gaa | 528 | | |
| Asp Gly Thr Val Phe Asp Ser Ser Tyr Asp Arg Gly Glu Pro Ile Glu | | | |
| 165 | 170 | 175 | |
| tcc caa tta aac caa tta att ccg ggt tgg att gaa gcg att cca atg | 576 | | |
| Phe Gln Leu Asn Gln Leu Ile Pro Gly Trp Ile Glu Ala Ile Pro Met | | | |
| 180 | 185 | 190 | |
| ttg aaa aaa ggc gga aaa atg gaa atc gtc gtt ccg cct gaa ctt ggt | 624 | | |
| Leu Lys Lys Gly Gly Lys Met Glu Ile Val Val Pro Pro Glu Leu Gly | | | |
| 195 | 200 | 205 | |
| tac ggc gaa cgc caa gca ggt aag att ccg gca agt tca acc tta aaa | 672 | | |
| Tyr Gly Glu Arg Gln Ala Gly Lys Ile Pro Ala Ser Ser Thr Leu Lys | | | |
| 210 | 215 | 220 | |
| ttc gag att gaa ttg tta gat ttc aaa gcg gcc gaa gcg aaa aaa taa | 720 | | |
| Phe Glu Ile Glu Leu Leu Asp Phe Lys Ala Ala Glu Ala Lys Lys | | | |
| 225 | 230 | 235 | |

<210> 143

<211> 239

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 143

| | | | |
|---|---|----|----|
| Met Leu Lys Asn Lys Leu Ser Val Leu Ala Ile Val Ala Gly Thr Phe | | | |
| 1 | 5 | 10 | 15 |

| | | | |
|---|----|----|--|
| Val Ser Ala Gln Thr Ala Phe Ala Ala Asp Gln Lys Phe Ile Asp Asp | | | |
| 20 | 25 | 30 | |

| | | | |
|---|----|----|--|
| Ser Ser Tyr Ala Val Gly Val Leu Met Gly Lys Asn Ile Glu Gly Val | | | |
| 35 | 40 | 45 | |

| | | | |
|---|----|----|--|
| Val Glu Ser Gln Lys Glu Ile Phe Ser Tyr Asn Gln Asp Lys Ile Leu | | | |
| 50 | 55 | 60 | |

| | | | |
|---|----|----|----|
| Ala Gly Val Gln Asp Thr Ile Lys Lys Thr Gly Lys Leu Thr Asp Glu | | | |
| 65 | 70 | 75 | 80 |

| | | | |
|---|----|----|--|
| Asp Leu Gln Lys Gln Leu Lys Ser Leu Asp Thr Tyr Leu Ala Ser Gln | | | |
| 85 | 90 | 95 | |

| | | | |
|---|-----|-----|--|
| Glu Ser Lys Ile Ala Ala Glu Lys Ser Lys Ala Thr Val Glu Ala Gly | | | |
| 100 | 105 | 110 | |

| | | | |
|---|-----|-----|--|
| Asn Lys Phe Arg Thr Asp Tyr Glu Lys Gln Ser Gly Val Lys Lys Thr | | | |
| 115 | 120 | 125 | |

| | | | |
|---|-----|-----|--|
| Ala Ser Gly Leu Leu Tyr Lys Ile Glu Lys Ala Gly Thr Gly Glu Ser | | | |
| 130 | 135 | 140 | |

| | | | |
|---|-----|-----|-----|
| Pro Lys Ala Glu Asp Thr Val Lys Val His Tyr Lys Gly Thr Leu Thr | | | |
| 145 | 150 | 155 | 160 |

Asp Gly Thr Val Phe Asp Ser Ser Tyr Asp Arg Gly Glu Pro Ile Glu
 165 170 175

Phe Gln Leu Asn Gln Leu Ile Pro Gly Trp Ile Glu Ala Ile Pro Met
 180 185 190

Leu Lys Lys Gly Gly Lys Met Glu Ile Val Val Pro Pro Glu Leu Gly
 195 200 205

Tyr Gly Glu Arg Gln Ala Gly Lys Ile Pro Ala Ser Ser Thr Leu Lys
 210 215 220

Phe Glu Ile Glu Leu Leu Asp Phe Lys Ala Ala Glu Ala Lys Lys
 225 230 235

<210> 144

<211> 290

<212> DNA

<213> *Actinobacillus pleuropneumoniae*

<220>

<223> HI0379

<220>

<221> CDS

<222> (3) .. (287)

<400> 144

tg cat agc gtg aga ggt ccg ggc ggc ggt tat caa ctc ggt aag caa 47
 His Ser Val Arg Gly Pro Gly Gly Tyr Gln Leu Gly Lys Gln
 1 5 10 15

cct gaa gag att agt gtg ggg atg att att gcg gcg gtg aat gaa aat 95
 Pro Glu Glu Ile Ser Val Gly Met Ile Ala Ala Val Asn Glu Asn
 20 25 30

ctc gac gta acc aaa tgt aaa ggt agc ggc aac tgc aat aac tct 143
 Leu Asp Val Thr Lys Cys Lys Gly Ser Gly Asn Cys Ser Lys Asn Ser
 35 40 45

cag tgc tta acc cat cat tta tgg gaa cgt tta gaa gaa caa atc ggt 191
 Gln Cys Leu Thr His His Leu Trp Glu Arg Leu Glu Glu Gln Ile Gly
 50 55 60

gtg ttt tta aat acg att act tta gcg gaa ctt gtt gaa gaa cat tcg 239
 Val Phe Leu Asn Thr Ile Thr Leu Ala Glu Leu Val Glu Glu His Ser
 65 70 75

gat cac gat tgt gaa aaa gaa cat tgc cac gat cat tca cac aaa cat 287
 Asp His Asp Cys Glu Lys Glu His Cys His Asp His Ser His Lys His
 80 85 90 95

taa 290

<210> 145

<211> 95

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 145

His Ser Val Arg Gly Pro Gly Gly Tyr Gln Leu Gly Lys Gln Pro

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1 | 5 | 10 | 15 | | | | | | | | | | | | |
| Glu | Glu | Ile | Ser | Val | Gly | Met | Ile | Ile | Ala | Ala | Val | Asn | Glu | Asn | Leu |
| | | | | 20 | | | | 25 | | | | | | | 30 |
| Asp | Val | Thr | Lys | Cys | Lys | Gly | Ser | Gly | Asn | Cys | Ser | Lys | Asn | Ser | Gln |
| | | | | | | | 35 | | 40 | | | 45 | | | |
| Cys | Leu | Thr | His | His | Leu | Trp | Glu | Arg | Leu | Glu | Glu | Gln | Ile | Gly | Val |
| | | | | | | | 50 | | 55 | | | 60 | | | |
| Phe | Leu | Asn | Thr | Ile | Thr | Leu | Ala | Glu | Leu | Val | Glu | Glu | His | Ser | Asp |
| | | | | | | | 65 | | 70 | | 75 | | | 80 | |
| His | Asp | Cys | Glu | Lys | Glu | His | Cys | His | Asp | His | Ser | His | Lys | His | |
| | | | | | | | 85 | | | 90 | | | 95 | | |

<210> 146

<211> 273

<212> DNA

<213> *Actinobacillus pleuropneumoniae*

<220>

<223> *hupA*

<220>

<221> CDS

<222> (1) .. (270)

<400> 146

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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| atg | aac | aaa | act | gag | tta | atc | gat | gca | atc | gca | gct | ggg | gca | gag | tta |
| Met | Asn | Lys | Thr | Glu | Leu | Ile | Asp | Ala | Ile | Ala | Ala | Gly | Ala | Glu | Leu |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| agc | aag | aaa | gac | gcg | aaa | gcg | gca | tta | gaa | gcg | act | tta | aat | gcg | atc |
| Ser | Lys | Lys | Asp | Ala | Lys | Ala | Ala | Leu | Glu | Ala | Thr | Leu | Asn | Ala | Ile |
| | | | | | | | 20 | | 25 | | | 30 | | | 96 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tct | gaa | agc | cta | aaa | aat | ggc | gac | acc | gtt | cag | tta | atc | ggc | ttc | ggg |
| Ser | Glu | Ser | Leu | Lys | Asn | Gly | Asp | Thr | Val | Gln | Leu | Ile | Gly | Phe | Gly |
| | | | | | | | 35 | | 40 | | | 45 | | | 144 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| act | ttt | aaa | gta | aac | gag | cgt | aat | gca | cgt | acg | ggg | cgt | aac | ccg | cgt |
| Thr | Phe | Lys | Val | Asn | Glu | Arg | Asn | Ala | Arg | Thr | Gly | Arg | Asn | Pro | Arg |
| | | | | | | | 50 | | 55 | | | 60 | | | 192 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| acc | ggc | gaa | gaa | atc | aaa | atc | gca | gca | tct | aaa | gtg | ccg | ggc | ttt | gtt |
| Thr | Gly | Glu | Ile | Lys | Ile | Ala | Ala | Ser | Lys | Val | Pro | Ala | Phe | Val | |
| | | | | | | | 65 | | 70 | | | 75 | | | 240 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|-----|
| gca | ggt | aaa | gca | tta | aaa | gat | tta | gta | aaa | taa | | | | | |
| Ala | Gly | Lys | Ala | Leu | Lys | Asp | Leu | Val | Lys | | | | | | 273 |
| | | | | | | 85 | | | 90 | | | | | | |

<210> 147

<211> 90

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 147

Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Gly Ala Glu Leu

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| 1 | 5 | 10 | 15 | | | | | | | | | | | | |
| Ser | Lys | Lys | Asp | Ala | Lys | Ala | Ala | Leu | Glu | Ala | Thr | Leu | Asn | Ala | Ile |
| | | | | 20 | | | | 25 | | | | | 30 | | |
| Ser | Glu | Ser | Leu | Lys | Asn | Gly | Asp | Thr | Val | Gln | Leu | Ile | Gly | Phe | Gly |
| | | | | 35 | | | 40 | | | | 45 | | | | |
| Thr | Phe | Lys | Val | Asn | Glu | Arg | Asn | Ala | Arg | Thr | Gly | Arg | Asn | Pro | Arg |
| | | | | 50 | | | 55 | | | 60 | | | | | |
| Thr | Gly | Glu | Glu | Ile | Lys | Ile | Ala | Ala | Ser | Lys | Val | Pro | Ala | Phe | Val |
| | | | | 65 | | | 70 | | | 75 | | | 80 | | |
| Ala | Gly | Lys | Ala | Leu | Lys | Asp | Leu | Val | Lys | | | | | | |
| | | | | 85 | | | 90 | | | | | | | | |

<210> 148
<211> 551
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>
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<220>
<221> CDS
<222> (1)..(549)

<400> 148
atg agc aaa gaa atc aaa acg caa gtc gtg gta ctt ggt gcg ggt cct 48
Met Ser Lys Glu Ile Lys Thr Gln Val Val Leu Gly Ala Gly Pro
1 5 10 15

gcc ggt tat tca gcg gca ttc cgt tgc ttt gcc gac tta ggc tta gaa aca 96
Ala Gly Tyr Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr
20 25 30

gta att gtc gaa cgt tat tca act ttg ggc ggt gta tgc tta aac gta 144
Val Ile Val Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val
35 40 45

ggt tgc att ccg tct aaa gca tta tca cac gtt gca aaa gtt atc gaa 192
Gly Cys Ile Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu
50 55 60

gaa gca aaa cac gca gag aaa aac ggt att act ttc ggt gag ccc aac 240
Glu Ala Lys His Ala Glu Lys Asn Gly Ile Thr Phe Gly Glu Pro Asn
65 70 75 80

att gat tta gat aaa gtg cgt gcg ggt aaa gaa gcg gtt gtt tct aaa 288
Ile Asp Leu Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys
85 90 95

tta acc ggc ggt tta gcg ggt atg gct aaa gca cgt aaa gta aca gta 336
Leu Thr Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val
100 105 110

gtg gaa ggt tta gcg gcg ttt acc gat ccg aat act tta gta gct cgt 384
Val Glu Gly Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg
115 120 125

| | | | |
|---|-----|-----|-----|
| gac cgt gac ggt aat ccg aca acg att aaa ttt gat tat gca att att | | 432 | |
| Asp Arg Asp Gly Asn Pro Thr Thr Ile Lys Phe Asp Tyr Ala Ile Ile | | | |
| 130 | 135 | 140 | |
| gca gcc ggt tct cgt ccg att cag ctt ccg ttc att cca cac gaa gat | | 480 | |
| Ala Ala Gly Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp | | | |
| 145 | 150 | 155 | 160 |
| ccg cgt gtg tgg gat tct acg gat gca ctt aaa tta aaa gaa gta ccc | | 528 | |
| Pro Arg Val Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro | | | |
| 165 | 170 | 175 | |
| gaa aaa att act cat tat ggg cc | | 551 | |
| Glu Lys Ile Thr His Tyr Gly | | | |
| 180 | | | |
|
 | | | |
| <210> 149 | | | |
| <211> 183 | | | |
| <212> PRT | | | |
| <213> <i>Actinobacillus pleuropneumoniae</i> | | | |
|
 | | | |
| <400> 149 | | | |
| Met Ser Lys Glu Ile Lys Thr Gln Val Val Val Leu Gly Ala Gly Pro | | | |
| 1 | 5 | 10 | 15 |
| Ala Gly Tyr Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr | | | |
| 20 | 25 | 30 | |
| Val Ile Val Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val | | | |
| 35 | 40 | 45 | |
| Gly Cys Ile Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu | | | |
| 50 | 55 | 60 | |
| Glu Ala Lys His Ala Glu Lys Asn Gly Ile Thr Phe Gly Glu Pro Asn | | | |
| 65 | 70 | 75 | 80 |
| Ile Asp Leu Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys | | | |
| 85 | 90 | 95 | |
| Leu Thr Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val | | | |
| 100 | 105 | 110 | |
| Val Glu Gly Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg | | | |
| 115 | 120 | 125 | |
| Asp Arg Asp Gly Asn Pro Thr Thr Ile Lys Phe Asp Tyr Ala Ile Ile | | | |
| 130 | 135 | 140 | |
| Ala Ala Gly Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp | | | |
| 145 | 150 | 155 | 160 |
| Pro Arg Val Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro | | | |
| 165 | 170 | 175 | |
| Glu Lys Ile Thr His Tyr Gly | | | |
| 180 | | | |
|
 | | | |
| <210> 150 | | | |
| <211> 1095 | | | |
| <212> DNA | | | |

<213> *Actinobacillus pleuropneumoniae*

<220>

<223> Omp5-2

<220>

<221> CDS

<222> (1) .. (1092)

<400> 150

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| atg | aaa | aaa | tca | tta | gtt | gct | tta | aca | gta | tta | tcg | gct | gca | gcg | gta | 48 |
| Met | Lys | Lys | Ser | Leu | Val | Ala | Leu | Thr | Val | Leu | Ser | Ala | Ala | Ala | Val | |
| 1 | | | | 5 | | | | 10 | | | | 15 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| gct | caa | gca | gcg | cca | caa | aat | act | ttc | tac | gca | ggt | gct | gca | aaa | gca | 96 |
| Ala | Gln | Ala | Ala | Pro | Gln | Gln | Asn | Thr | Phe | Tyr | Ala | Gly | Ala | Lys | Ala | |
| 20 | | | | 25 | | | | 30 | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ggt | tgg | gct | tca | ttc | cat | gat | ggt | atc | gaa | caa | tta | gat | tca | gct | aaa | 144 |
| Gly | Trp | Ala | Ser | Phe | His | Asp | Gly | Ile | Glu | Gln | Leu | Asp | Ser | Ala | Lys | |
| 35 | | | | 40 | | | 45 | | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aac | aca | gat | cgc | ggt | aca | aaa | tac | ggt | atc | aac | cgt | aat | tca | gta | act | 192 |
| Asn | Thr | Asp | Arg | Gly | Thr | Lys | Tyr | Gly | Ile | Asn | Arg | Asn | Ser | Val | Thr | |
| 50 | | | | 55 | | | 60 | | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tac | ggc | gta | ttc | ggc | ggt | tac | caa | att | tta | aac | caa | gac | aaa | tta | ggt | 240 |
| Tyr | Gly | Val | Phe | Gly | Tyr | Gln | Ile | Leu | Asn | Gln | Asp | Lys | Leu | Gly | | |
| 65 | | | 70 | | | 75 | | 80 | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| tta | gct | gaa | tta | ggt | tat | gac | tat | ttc | ggt | cgt | gtg | cgc | ggt | tct | 288 | |
| Leu | Ala | Ala | Glu | Leu | Gly | Tyr | Asp | Tyr | Phe | Gly | Arg | Val | Arg | Gly | Ser | |
| 85 | | | 90 | | | 95 | | | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gaa | aaa | cca | aac | ggt | aaa | gct | gac | aag | aaa | act | ttc | cgt | cac | gct | gca | 336 |
| Glu | Lys | Pro | Asn | Gly | Lys | Ala | Asp | Lys | Lys | Thr | Phe | Arg | His | Ala | Ala | |
| 100 | | | | 105 | | | 110 | | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| cac | ggt | gct | aca | atc | gca | tta | aaa | cct | agc | tac | gaa | gta | tta | cct | gac | 384 |
| His | Gly | Ala | Thr | Ile | Ala | Leu | Lys | Pro | Ser | Tyr | Glu | Val | Leu | Pro | Asp | |
| 115 | | | 120 | | | 125 | | | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tta | gac | gtt | tac | ggt | aaa | gta | ggt | atc | gca | tta | gta | aac | aat | aca | tat | 432 |
| Leu | Asp | Val | Tyr | Gly | Lys | Val | Gly | Ile | Ala | Leu | Val | Asn | Asn | Thr | Tyr | |
| 130 | | | 135 | | | 140 | | | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aaa | aca | ttc | aat | gca | gca | caa | gag | aaa | gtg | aaa | act | cgt | cgt | ttc | caa | 480 |
| Lys | Thr | Phe | Asn | Ala | Ala | Gln | Glu | Lys | Val | Lys | Thr | Arg | Arg | Phe | Gln | |
| 145 | | | 150 | | | 155 | | 160 | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| agt | tct | tta | att | tta | ggt | gct | ggt | gtt | gag | tac | gca | att | ctt | cct | gaa | 528 |
| Ser | Ser | Leu | Ile | Leu | Gly | Ala | Gly | Val | Glu | Tyr | Ala | Ile | Leu | Pro | Glu | |
| 165 | | | 170 | | | 175 | | | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tta | gct | gca | cgt | gtt | gaa | tac | caa | tgg | tta | aac | aac | gca | ggt | aaa | gca | 576 |
| Leu | Ala | Ala | Arg | Val | Glu | Tyr | Gln | Trp | Leu | Asn | Asn | Ala | Gly | Lys | Ala | |
| 180 | | | 185 | | | 190 | | | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| agc | tac | tct | act | tta | aat | cgt | atg | ggt | gca | act | gac | tac | cgt | tcg | gat | 624 |
| Ser | Tyr | Ser | Thr | Leu | Asn | Arg | Met | Gly | Ala | Thr | Asp | Tyr | Arg | Ser | Asp | |
| 195 | | | 200 | | | 205 | | | | | | | | | | |

| | |
|---|------|
| atc agt tcc gta tct gca ggt tta agc tac cgt ttc ggt caa ggt gcg
Ile Ser Ser Val Ser Ala Gly Leu Ser Tyr Arg Phe Gly Gln Gly Ala
210 215 220 | 672 |
| gca ccg gtt gca gct ccg gca gtt gaa act aaa aac ttc gca ttc agc
Ala Pro Val Ala Ala Pro Ala Val Glu Thr Lys Asn Phe Ala Phe Ser
225 230 235 240 | 720 |
| tct gac gta tta ttc gca ttc ggt aaa tca aac tta aaa ccg gct gcg
Ser Asp Val Leu Phe Ala Phe Gly Lys Ser Asn Leu Lys Pro Ala Ala
245 250 255 | 768 |
| gca aca gca tta gat gca atg caa acc gaa atc aat aac gca ggt tta
Ala Thr Ala Leu Asp Ala Met Gln Thr Glu Ile Asn Asn Ala Gly Leu
260 265 270 | 816 |
| tca aat gct gcg atc caa gta aac ggt tac acg gac cgt atc ggt aaa
Ser Asn Ala Ala Ile Gln Val Asn Gly Tyr Thr Asp Arg Ile Gly Lys
275 280 285 | 864 |
| gaa gct tca aac tta aaa ctt tca caa cgt cgt gcg gaa aca gta gct
Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg Ala Glu Thr Val Ala
290 295 300 | 912 |
| aac tac atc gtt tct aaa ggt gct ccg gca gct aac gta act gca gta
Asn Tyr Ile Val Ser Lys Gly Ala Pro Ala Ala Asn Val Thr Ala Val
305 310 315 320 | 960 |
| ggg tac ggt gaa gca aac cct gta acc ggc gca aca tgt gac aaa gtt
Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala Thr Cys Asp Lys Val
325 330 335 | 1008 |
| aaa ggt cgt aaa gca tta atc gct tgc tta gca ccg gat cgt cgt gtt
Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala Pro Asp Arg Arg Val
340 345 350 | 1056 |
| gaa gtt caa gtt caa ggt act aaa gaa gta act atg taa
Glu Val Gln Val Gln Gly Thr Lys Glu Val Thr Met
355 360 | 1095 |

<210> 151
<211> 364
<212> PRT
<213> *Actinobacillus pleuropneumoniae*

<400> 151
Met Lys Lys Ser Leu Val Ala Leu Thr Val Leu Ser Ala Ala Ala Val
1 5 10 15

Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Ala
20 25 30

Gly Trp Ala Ser Phe His Asp Gly Ile Glu Gln Leu Asp Ser Ala Lys
35 40 45

Asn Thr Asp Arg Gly Thr Lys Tyr Gly Ile Asn Arg Asn Ser Val Thr
50 55 60

Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asp Lys Leu Gly
65 70 75 80

Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Phe Gly Arg Val Arg Gly Ser

| 85 | 90 | 95 |
|---|---------------------------------|-----|
| Glu Lys Pro Asn Gly Lys Ala Asp | Lys Lys Thr Phe Arg His Ala Ala | |
| 100 | 105 | 110 |
| His Gly Ala Thr Ile Ala Leu Lys | Pro Ser Tyr Glu Val Leu Pro Asp | |
| 115 | 120 | 125 |
| Leu Asp Val Tyr Gly Lys Val Gly Ile Ala Leu Val Asn Asn Thr Tyr | | |
| 130 | 135 | 140 |
| Lys Thr Phe Asn Ala Ala Gln Glu Lys Val Lys Thr Arg Arg Phe Gln | | |
| 145 | 150 | 155 |
| 160 | | |
| Ser Ser Leu Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro Glu | | |
| 165 | 170 | 175 |
| Leu Ala Ala Arg Val Glu Tyr Gln Trp Leu Asn Asn Ala Gly Lys Ala | | |
| 180 | 185 | 190 |
| Ser Tyr Ser Thr Leu Asn Arg Met Gly Ala Thr Asp Tyr Arg Ser Asp | | |
| 195 | 200 | 205 |
| Ile Ser Ser Val Ser Ala Gly Leu Ser Tyr Arg Phe Gly Gln Gly Ala | | |
| 210 | 215 | 220 |
| Ala Pro Val Ala Ala Pro Ala Val Glu Thr Lys Asn Phe Ala Phe Ser | | |
| 225 | 230 | 235 |
| 240 | | |
| Ser Asp Val Leu Phe Ala Phe Gly Lys Ser Asn Leu Lys Pro Ala Ala | | |
| 245 | 250 | 255 |
| Ala Thr Ala Leu Asp Ala Met Gln Thr Glu Ile Asn Asn Ala Gly Leu | | |
| 260 | 265 | 270 |
| Ser Asn Ala Ala Ile Gln Val Asn Gly Tyr Thr Asp Arg Ile Gly Lys | | |
| 275 | 280 | 285 |
| Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg Ala Glu Thr Val Ala | | |
| 290 | 295 | 300 |
| Asn Tyr Ile Val Ser Lys Gly Ala Pro Ala Ala Asn Val Thr Ala Val | | |
| 305 | 310 | 315 |
| 320 | | |
| Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala Thr Cys Asp Lys Val | | |
| 325 | 330 | 335 |
| Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala Pro Asp Arg Arg Val | | |
| 340 | 345 | 350 |
| Glu Val Gln Val Gln Gly Thr Lys Glu Val Thr Met | | |
| 355 | 360 | |

<210> 152
<211> 1110
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>
<223> Omp5

<220>

<221> CDS

<222> (1)..(1107)

<400> 152

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| atg | aaa | aaa | tca | tta | gtt | gct | tta | gca | gta | tta | tcg | gct | gca | gca | gta | 48 |
| Met | Lys | Lys | Ser | Leu | Val | Ala | Leu | Ala | Val | Leu | Ser | Ala | Ala | Ala | Val | |
| 1 | | | | 5 | | | | 10 | | | | 15 | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|
| gct | caa | gca | gct | cca | caa | aat | act | ttc | tac | gca | ggt | gct | gca | aaa | gtt | 96 |
| Ala | Gln | Ala | Ala | Pro | Gln | Gln | Asn | Thr | Phe | Tyr | Ala | Gly | Ala | Lys | Val | |
| 20 | | | | 25 | | | | 30 | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| ggt | caa | tca | tca | ttt | cac | cac | ggt | gtt | aac | caa | tta | aaa | tct | ggt | cac | 144 |
| Gly | Gln | Ser | Ser | Phe | His | His | Gly | Val | Asn | Gln | Leu | Lys | Ser | Gly | His | |
| 35 | | | | 40 | | | 45 | | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gat | gat | cgt | tat | aat | gat | aaa | aca | cgt | aag | tat | ggt | atc | aac | cgt | aac | 192 |
| Asp | Asp | Arg | Tyr | Asn | Asp | Lys | Thr | Arg | Lys | Tyr | Gly | Ile | Asn | Arg | Asn | |
| 50 | | | | 55 | | | 60 | | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tct | gta | act | tac | ggt | gta | ttc | ggc | ggt | tac | caa | atc | tta | aac | caa | aat | 240 |
| Ser | Val | Thr | Tyr | Gly | Val | Phe | Gly | Gly | Tyr | Gln | Ile | Leu | Asn | Gln | Asn | |
| 65 | | | | 70 | | | 75 | | | 80 | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aac | ttc | ggt | tta | gca | gct | gaa | tta | ggc | tat | gac | tac | tac | ggt | cgc | gta | 288 |
| Asn | Phe | Gly | Leu | Ala | Ala | Glu | Leu | Gly | Tyr | Asp | Tyr | Tyr | Gly | Arg | Val | |
| 85 | | | | 90 | | | 95 | | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| cgt | ggt | aac | gta | gat | gaa | ttc | cgt | aca | gtt | aaa | cac | tct | gct | cac | ggt | 336 |
| Arg | Gly | Asn | Val | Asp | Glu | Phe | Arg | Thr | Val | Lys | His | Ser | Ala | His | Gly | |
| 100 | | | | 105 | | | 110 | | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tta | aac | tta | gcg | tta | aaa | cca | agc | tac | gaa | gta | tta | cct | gac | tta | gac | 384 |
| Leu | Asn | Leu | Ala | Leu | Lys | Pro | Ser | Tyr | Glu | Val | Leu | Pro | Asp | Leu | Asp | |
| 115 | | | | 120 | | | 125 | | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gtt | tac | ggt | aaa | gta | ggt | att | gcg | gtt | gtt | cgt | aat | gac | tat | aaa | aaa | 432 |
| Val | Tyr | Gly | Lys | Val | Gly | Ile | Ala | Val | Val | Arg | Asn | Asp | Tyr | Lys | Lys | |
| 130 | | | | 135 | | | 140 | | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tat | ggt | gct | gaa | aac | act | aac | gaa | tca | aca | aca | aaa | ttc | cac | aaa | tta | 480 |
| Tyr | Gly | Ala | Glu | Asn | Thr | Asn | Glu | Ser | Thr | Thr | Lys | Phe | His | Lys | Leu | |
| 145 | | | | 150 | | | 155 | | | 160 | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| aaa | gca | tca | act | att | tta | ggt | gca | ggt | gtt | gag | tac | gca | att | ctt | cct | 528 |
| Lys | Ala | Ser | Thr | Ile | Leu | Gly | Ala | Gly | Val | Glu | Tyr | Ala | Ile | Leu | Pro | |
| 165 | | | | 170 | | | 175 | | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| gaa | tta | gct | gca | cgt | ggt | gaa | tac | caa | tac | tta | aac | aaa | gct | ggg | aac | 576 |
| Glu | Leu | Ala | Ala | Arg | Val | Glu | Tyr | Gln | Tyr | Leu | Asn | Lys | Ala | Gly | Asn | |
| 180 | | | | 185 | | | 190 | | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tta | aat | aaa | gca | tta | gtt | cgt | tca | ggc | aca | caa | gat | gtt | gac | ttc | caa | 624 |
| Leu | Asn | Lys | Ala | Leu | Val | Arg | Ser | Gly | Thr | Gln | Asp | Val | Asp | Phe | Gln | |
| 195 | | | | 200 | | | 205 | | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tat | gct | cct | gat | atc | cac | tct | gta | aca | gca | ggt | tta | tca | tac | cgt | ttc | 672 |
| Tyr | Ala | Pro | Asp | Ile | His | Ser | Val | Thr | Ala | Gly | Leu | Ser | Tyr | Arg | Phe | |
| 210 | | | | 215 | | | 220 | | | | | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| ggt | caa | ggc | gct | gta | gca | cca | gtt | gag | cca | gaa | gtt | gta | act | aaa | 720 | |
| Gly | Gln | Gly | Ala | Val | Ala | Pro | Val | Val | Glu | Pro | Glu | Val | Val | Thr | Lys | |
| 225 | | | | 230 | | | 235 | | | 240 | | | | | | |

| | | | |
|---|------|-----|-----|
| aac ttc gca ttc agc tca gac gtt tta ttt gat ttc ggt aaa tca agc | 768 | | |
| Asn Phe Ala Phe Ser Ser Asp Val Leu Phe Asp Phe Gly Lys Ser Ser | | | |
| 245 | 250 | 255 | |
| tta aaa cca gca gca aca gct tta gac gca gct aac act gaa atc | 816 | | |
| Leu Lys Pro Ala Ala Ala Thr Ala Leu Asp Ala Ala Asn Thr Glu Ile | | | |
| 260 | 265 | 270 | |
| gct aac tta ggt tta gca act cca gct atc caa gtt aac ggt tat aca | 864 | | |
| Ala Asn Leu Gly Leu Ala Thr Pro Ala Ile Gln Val Asn Gly Tyr Thr | | | |
| 275 | 280 | 285 | |
| gac cgt atc ggt aaa gaa gct tca aac tta aaa ctt tca caa cgc cgt | 912 | | |
| Asp Arg Ile Gly Lys Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg | | | |
| 290 | 295 | 300 | |
| gca gaa act gta gct aac tac tta gtt tct aaa ggt caa aac cct gca | 960 | | |
| Ala Glu Thr Val Ala Asn Tyr Leu Val Ser Lys Gly Gln Asn Pro Ala | | | |
| 305 | 310 | 315 | 320 |
| aac gta act gca gta ggt tac ggt gaa gca aac cca gta acc ggc gca | 1008 | | |
| Asn Val Thr Ala Val Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala | | | |
| 325 | 330 | 335 | |
| aca tgt gat gca gtt aaa ggt cgt aaa gca tta atc gct tgc tta gca | 1056 | | |
| Thr Cys Asp Ala Val Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala | | | |
| 340 | 345 | 350 | |
| ccg gat cgt cgt gtt gaa gtt caa gta caa ggt gct aaa aac gta gct | 1104 | | |
| Pro Asp Arg Arg Val Glu Val Gln Val Gln Gly Ala Lys Asn Val Ala | | | |
| 355 | 360 | 365 | |
| atg taa | 1110 | | |
| Met | | | |

<210> 153

<211> 369

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 153

Met Lys Lys Ser Leu Val Ala Leu Ala Val Leu Ser Ala Ala Ala Val

1 5 10 15

Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Val

20 25 30

Gly Gln Ser Ser Phe His His Gly Val Asn Gln Leu Lys Ser Gly His

35 40 45

Asp Asp Arg Tyr Asn Asp Lys Thr Arg Lys Tyr Gly Ile Asn Arg Asn

50 55 60

Ser Val Thr Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asn

65 70 75 80

Asn Phe Gly Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Tyr Gly Arg Val

85 90 95

Arg Gly Asn Val Asp Glu Phe Arg Thr Val Lys His Ser Ala His Gly

100 105 110

Leu Asn Leu Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp Leu Asp
 115 120 125
 Val Tyr Gly Lys Val Gly Ile Ala Val Val Arg Asn Asp Tyr Lys Lys
 130 135 140
 Tyr Gly Ala Glu Asn Thr Asn Glu Ser Thr Thr Lys Phe His Lys Leu
 145 150 155 160
 Lys Ala Ser Thr Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro
 165 170 175
 Glu Leu Ala Ala Arg Val Glu Tyr Gln Tyr Leu Asn Lys Ala Gly Asn
 180 185 190
 Leu Asn Lys Ala Leu Val Arg Ser Gly Thr Gln Asp Val Asp Phe Gln
 195 200 205
 Tyr Ala Pro Asp Ile His Ser Val Thr Ala Gly Leu Ser Tyr Arg Phe
 210 215 220
 Gly Gln Gly Ala Val Ala Pro Val Val Glu Pro Glu Val Val Thr Lys
 225 230 235 240
 Asn Phe Ala Phe Ser Ser Asp Val Leu Phe Asp Phe Gly Lys Ser Ser
 245 250 255
 Leu Lys Pro Ala Ala Ala Thr Ala Leu Asp Ala Ala Asn Thr Glu Ile
 260 265 270
 Ala Asn Leu Gly Leu Ala Thr Pro Ala Ile Gln Val Asn Gly Tyr Thr
 275 280 285
 Asp Arg Ile Gly Lys Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg
 290 295 300
 Ala Glu Thr Val Ala Asn Tyr Leu Val Ser Lys Gly Gln Asn Pro Ala
 305 310 315 320
 Asn Val Thr Ala Val Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala
 325 330 335
 Thr Cys Asp Ala Val Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala
 340 345 350
 Pro Asp Arg Arg Val Glu Val Gln Val Gln Gly Ala Lys Asn Val Ala
 355 360 365

Met

<210> 154
 <211> 1076
 <212> DNA
 <213> *Actinobacillus pleuropneumoniae*
 <220>
 <223> pnp new
 <220>
 <221> CDS
 <222> (1)..(1074)

<400> 154
 aat att aaa gaa ttc gta aaa gaa gcg ggt aaa ccg cgt tgg gat tgg 48
 Asn Ile Lys Glu Phe Val Lys Glu Ala Gly Lys Pro Arg Trp Asp Trp
 1 5 10 15

gtt gcg ccg gaa ccg aat acc gca tta atc aac caa gtt aaa gcg tta 96
 Val Ala Pro Glu Pro Asn Thr Ala Leu Ile Asn Gln Val Lys Ala Leu
 20 25 30

gct gaa gct cgt atc ggc gat ccg tat cgt att aca gaa aaa caa gct 144
 Ala Glu Ala Arg Ile Gly Asp Ala Tyr Arg Ile Thr Glu Lys Gln Ala
 35 40 45

cgt tac gaa caa atc gat gca att aaa gct gat gtt atc gca caa tta 192
 Arg Tyr Glu Gln Ile Asp Ala Ile Lys Ala Asp Val Ile Ala Gln Leu
 50 55 60

acc gca caa gac gaa acc gtt tct gaa ggt gct att att gat att att 240
 Thr Ala Gln Asp Glu Thr Val Ser Glu Gly Ala Ile Ile Asp Ile Ile
 65 70 75 80

acc gca tta gaa agt tct att gtt cgc ggt cgt att att gcc ggc gaa 288
 Thr Ala Leu Glu Ser Ser Ile Val Arg Gly Arg Ile Ile Ala Gly Glu
 85 90 95

ccg cgt att gac ggt cgt acg gta gat acg gtt cgt gca tta gac att 336
 Pro Arg Ile Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile
 100 105 110

tgc acc ggc gta tta cct cgt acg cac ggt tct gca atc ttt act cgc 384
 Cys Thr Gly Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg
 115 120 125

ggt gaa aca caa gca tta gct gta acc tta ggt act gag cgc gat 432
 Gly Glu Thr Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp
 130 135 140

gca caa att gtt gac gaa tta acc ggc gag aaa tca gac cgt ttc tta 480
 Ala Gln Ile Val Asp Glu Leu Thr Gly Glu Lys Ser Asp Arg Phe Leu
 145 150 155 160

ttc cac tat aac ttc cct ccg tac tct gtc ggt gaa acc ggt cgt atc 528
 Phe His Tyr Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Arg Ile
 165 170 175

ggt tcg ccg aaa cgt cgt gaa atc ggc cac ggt cgt tta gct aaa cgc 576
 Gly Ser Pro Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg
 180 185 190

ggt gta tta gct gta atg ccg act gct gaa gaa ttc ccg tat gta gtg 624
 Gly Val Leu Ala Val Met Pro Thr Ala Glu Glu Phe Pro Tyr Val Val
 195 200 205

ccg gta gta tct gaa att acc gaa tca aac ggt tct tct tca atg gct 672
 Arg Val Val Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala
 210 215 220

tcc gta tgc ggc gca tct tta gct gaa atg gac gca ggc gta ccg att 720
 Ser Val Cys Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile
 225 230 235 240

aaa gct gct ggt gct ggt atc gca atg ggc tta gtg aaa gaa gaa gaa 768
 Lys Ala Ala Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Glu Glu

| 245 | 250 | 255 | |
|--|-----|-----|------|
| aaa ttt gtg gtg ctt tca gac atc tta ggt gac gaa gac cat tta ggc
Lys Phe Val Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly | 260 | 265 | 816 |
| gat atg gac ttc aaa gta gcc ggt acg cgt gaa ggt gta acc gca ctt
Asp Met Asp Phe Lys Val Ala Gly Thr Arg Glu Gly Val Thr Ala Leu | 275 | 280 | 864 |
| caa atg gat att aaa atc gaa ggt atc acg cct gaa att atg caa atc
Gln Met Asp Ile Lys Ile Glu Gly Ile Thr Pro Glu Ile Met Gln Ile | 290 | 295 | 912 |
| gca tta aat caa gcg aaa ggt gcg cgt atg cac atc tta agc gtg atg
Ala Leu Asn Gln Ala Lys Gly Ala Arg Met His Ile Leu Ser Val Met | 305 | 310 | 960 |
| gaa caa gcg att cct gca cct cgt gcc gat att tcc gat ttt gcg cct
Glu Gin Ala Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro | 325 | 330 | 1008 |
| cgt att cat acg atg aag atc gat ccg aag aaa atc aaa gac gtg atc
Arg Ile His Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile | 340 | 345 | 1056 |
| ggt aaa ggc ggt gcg gtt at
Gly Lys Gly Gly Ala Val | 355 | | 1076 |
|
<210> 155 | | | |
| <211> 358 | | | |
| <212> PRT | | | |
| <213> Actinobacillus pleuropneumoniae | | | |
|
<400> 155 | | | |
| Asn Ile Lys Glu Phe Val Lys Glu Ala Gly Lys Pro Arg Trp Asp Trp | 1 | 5 | 10 |
| | | | 15 |
| Val Ala Pro Glu Pro Asn Thr Ala Leu Ile Asn Gln Val Lys Ala Leu | 20 | 25 | 30 |
| | | | |
| Ala Glu Ala Arg Ile Gly Asp Ala Tyr Arg Ile Thr Glu Lys Gln Ala | 35 | 40 | 45 |
| | | | |
| Arg Tyr Glu Gln Ile Asp Ala Ile Lys Ala Asp Val Ile Ala Gln Leu | 50 | 55 | 60 |
| | | | |
| Thr Ala Gln Asp Glu Thr Val Ser Glu Gly Ala Ile Ile Asp Ile Ile | 65 | 70 | 75 |
| | | | 80 |
| | | | |
| Thr Ala Leu Glu Ser Ser Ile Val Arg Gly Arg Ile Ile Ala Gly Glu | 85 | 90 | 95 |
| | | | |
| Pro Arg Ile Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile | 100 | 105 | 110 |
| | | | |
| Cys Thr Gly Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg | 115 | 120 | 125 |
| | | | |
| Gly Glu Thr Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp | | | |

| 130 | 135 | 140 |
|---|-----|-----|
| Ala Gln Ile Val Asp Glu Leu Thr Gly Glu Lys Ser Asp Arg Phe Leu | | |
| 145 | 150 | 155 |
| Phe His Tyr Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Arg Ile | | |
| 165 | 170 | 175 |
| Gly Ser Pro Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg | | |
| 180 | 185 | 190 |
| Gly Val Leu Ala Val Met Pro Thr Ala Glu Glu Phe Pro Tyr Val Val | | |
| 195 | 200 | 205 |
| Arg Val Val Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala | | |
| 210 | 215 | 220 |
| Ser Val Cys Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile | | |
| 225 | 230 | 235 |
| Lys Ala Ala Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Glu | | |
| 245 | 250 | 255 |
| Lys Phe Val Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly | | |
| 260 | 265 | 270 |
| Asp Met Asp Phe Lys Val Ala Gly Thr Arg Glu Gly Val Thr Ala Leu | | |
| 275 | 280 | 285 |
| Gln Met Asp Ile Lys Ile Glu Gly Ile Thr Pro Glu Ile Met Gln Ile | | |
| 290 | 295 | 300 |
| Ala Leu Asn Gln Ala Lys Gly Ala Arg Met His Ile Leu Ser Val Met | | |
| 305 | 310 | 315 |
| Glu Gln Ala Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro | | |
| 325 | 330 | 335 |
| Arg Ile His Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile | | |
| 340 | 345 | 350 |
| Gly Lys Gly Gly Ala Val | | |
| 355 | | |

<210> 156
<211> 1055
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>
<223> potD

<220>
<221> CDS
<222> (1)..(1053)

<400> 156
atg aaa aaa tta gcg ggt tta ttt gca gca ggt tta gcg aca gtt gca 48
Met Lys Lys Leu Ala Gly Leu Phe Ala Ala Gly Leu Ala Thr Val Ala
1 5 10 15

tta aca gcg tgt aat gaa gaa aag cca aaa gcg gct gaa gca gcg gct 96

| | | | |
|---|-----|-----|-----|
| Leu Thr Ala Cys Asn Glu Glu Lys Pro Lys Ala Ala Glu Ala Ala Ala | | | |
| 20 | 25 | 30 | |
| caa ccg gca gca gcg gga aca gtt cac ctt tat act tgg act gaa tat | | | 144 |
| Gln Pro Ala Ala Ala Gly Thr Val His Leu Tyr Thr Trp Thr Glu Tyr | | | |
| 35 | 40 | 45 | |
| gtg cct gaa ggc ttg tta gat gaa ttt aca aag caa acc ggt atc aaa | | | 192 |
| Val Pro Glu Gly Leu Leu Asp Glu Phe Thr Lys Gln Thr Gly Ile Lys | | | |
| 50 | 55 | 60 | |
| gta gag gtt tca agc ctt gaa tct aac gaa acc atg tat gcg aaa tta | | | 240 |
| Val Glu Val Ser Ser Leu Glu Ser Asn Glu Thr Met Tyr Ala Lys Leu | | | |
| 65 | 70 | 75 | 80 |
| aaa tta caa ggt aaa gac ggc ggt tac gat gtt atc gca cct tct aac | | | 288 |
| Lys Leu Gln Gly Lys Asp Gly Gly Tyr Asp Val Ile Ala Pro Ser Asn | | | |
| 85 | 90 | 95 | |
| tac ttc gtt tca aaa atg gcg aaa gaa ggt atg tta gcg gaa tta gat | | | 336 |
| Tyr Phe Val Ser Lys Met Ala Lys Glu Gly Met Leu Ala Glu Leu Asp | | | |
| 100 | 105 | 110 | |
| cac gca aaa ctt cct gta atc aaa gag tta aac caa gat tgg tta aac | | | 384 |
| His Ala Lys Leu Pro Val Ile Lys Glu Leu Asn Gln Asp Trp Leu Asn | | | |
| 115 | 120 | 125 | |
| aaa cct tat gac caa ggt aac aaa tac tct tta ccg caa tta tta ggt | | | 432 |
| Lys Pro Tyr Asp Gln Gly Asn Lys Tyr Ser Leu Pro Gln Leu Leu Gly | | | |
| 130 | 135 | 140 | |
| gca ccg ggt atc gca ttt aac tca aat gac tat aag ggc gat gcg ttc | | | 480 |
| Ala Pro Gly Ile Ala Phe Asn Ser Asn Asp Tyr Lys Gly Asp Ala Phe | | | |
| 145 | 150 | 155 | 160 |
| act tct tgg ggt gat tta tgg aaa cct gag ttt gcg aat aaa gta caa | | | 528 |
| Thr Ser Trp Gly Asp Leu Trp Lys Pro Glu Phe Ala Asn Lys Val Gln | | | |
| 165 | 170 | 175 | |
| tta tta gat gac gca cgt gaa gta ttt aac att gcg tta tta aaa tta | | | 576 |
| Leu Leu Asp Asp Ala Arg Glu Val Phe Asn Ile Ala Leu Leu Lys Leu | | | |
| 180 | 185 | 190 | |
| ggt aaa aac cct aat aca acc aat ccg gaa gag att aaa gcg gct tac | | | 624 |
| Gly Lys Asn Pro Asn Thr Thr Asn Pro Glu Glu Ile Lys Ala Ala Tyr | | | |
| 195 | 200 | 205 | |
| gaa gag tta aga aaa tta cgt cca aac gta ctt tct ttc act tca gac | | | 672 |
| Glu Glu Leu Arg Lys Leu Arg Pro Asn Val Leu Ser Phe Thr Ser Asp | | | |
| 210 | 215 | 220 | |
| aac cca gcg aac tca ttt atc gca ggt gaa gta tct gta ggt caa tta | | | 720 |
| Asn Pro Ala Asn Ser Phe Ile Ala Gly Glu Val Ser Val Gly Gln Leu | | | |
| 225 | 230 | 235 | 240 |
| tgg aac ggt tct gta cgt att gcg aaa aaa gaa caa gcg ccg gta aac | | | 768 |
| Trp Asn Gly Ser Val Arg Ile Ala Lys Lys Glu Gln Ala Pro Val Asn | | | |
| 245 | 250 | 255 | |
| atg gtg ttc cca aaa gaa ggt cct gta ctt tgg gtt gat acg tta gcc | | | 816 |
| Met Val Phe Pro Lys Glu Gly Pro Val Leu Trp Val Asp Thr Leu Ala | | | |

260

265

270

att ccg gcg aat gcg aaa aac aaa gaa aat gcg cat aag tta atc aac 864
 Ile Pro Ala Asn Ala Lys Asn Lys Glu Asn Ala His Lys Leu Ile Asn
 275 280 285

tac tta tta agc gca ccg gtt gcg gaa aaa tta acg tta gaa atc ggt 912
 Tyr Leu Leu Ser Ala Pro Val Ala Glu Lys Leu Thr Leu Glu Ile Gly
 290 295 300

tat ccg act tca aac gta gaa gcg tta aaa aca tta cca aaa gag att 960
 Tyr Pro Thr Ser Asn Val Glu Ala Leu Lys Thr Leu Pro Lys Glu Ile
 305 310 315 320

acc gaa gat ccg gca atc tat ccg aca gct gat gtg tta aaa gcg gca 1008
 Thr Glu Asp Pro Ala Ile Tyr Pro Thr Ala Asp Val Leu Lys Ala Ala
 325 330 335

caa tgg caa gac gat gta ggt aat gca atc gaa ctt tac gaa aaa ta 1055
 Gln Trp Gln Asp Asp Val Gly Asn Ala Ile Glu Leu Tyr Glu Lys
 340 345 350

<210> 157

<211> 351

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 157

Met Lys Lys Leu Ala Gly Leu Phe Ala Ala Gly Leu Ala Thr Val Ala
 1 5 10 15

Leu Thr Ala Cys Asn Glu Glu Lys Pro Lys Ala Ala Glu Ala Ala Ala
 20 25 30

Gln Pro Ala Ala Ala Gly Thr Val His Leu Tyr Thr Trp Thr Glu Tyr
 35 40 45

Val Pro Glu Gly Leu Leu Asp Glu Phe Thr Lys Gln Thr Gly Ile Lys
 50 55 60

Val Glu Val Ser Ser Leu Glu Ser Asn Glu Thr Met Tyr Ala Lys Leu
 65 70 75 80

Lys Leu Gln Gly Lys Asp Gly Gly Tyr Asp Val Ile Ala Pro Ser Asn
 85 90 95

Tyr Phe Val Ser Lys Met Ala Lys Glu Gly Met Leu Ala Glu Leu Asp
 100 105 110

His Ala Lys Leu Pro Val Ile Lys Glu Leu Asn Gln Asp Trp Leu Asn
 115 120 125

Lys Pro Tyr Asp Gln Gly Asn Lys Tyr Ser Leu Pro Gln Leu Leu Gly
 130 135 140

Ala Pro Gly Ile Ala Phe Asn Ser Asn Asp Tyr Lys Gly Asp Ala Phe
 145 150 155 160

Thr Ser Trp Gly Asp Leu Trp Lys Pro Glu Phe Ala Asn Lys Val Gln
 165 170 175

Leu Leu Asp Asp Ala Arg Glu Val Phe Asn Ile Ala Leu Leu Lys Leu

| | | |
|---|-----|-----|
| 180 | 185 | 190 |
| Gly Lys Asn Pro Asn Thr Thr Asn Pro Glu Glu Ile Lys Ala Ala Tyr | | |
| 195 | 200 | 205 |
| Glu Glu Leu Arg Lys Leu Arg Pro Asn Val Leu Ser Phe Thr Ser Asp | | |
| 210 | 215 | 220 |
| Asn Pro Ala Asn Ser Phe Ile Ala Gly Glu Val Ser Val Gly Gln Leu | | |
| 225 | 230 | 235 |
| Trp Asn Gly Ser Val Arg Ile Ala Lys Lys Glu Gln Ala Pro Val Asn | | |
| 245 | 250 | 255 |
| Met Val Phe Pro Lys Glu Gly Pro Val Leu Trp Val Asp Thr Leu Ala | | |
| 260 | 265 | 270 |
| Ile Pro Ala Asn Ala Lys Asn Lys Glu Asn Ala His Lys Leu Ile Asn | | |
| 275 | 280 | 285 |
| Tyr Leu Leu Ser Ala Pro Val Ala Glu Lys Leu Thr Leu Glu Ile Gly | | |
| 290 | 295 | 300 |
| Tyr Pro Thr Ser Asn Val Glu Ala Leu Lys Thr Leu Pro Lys Glu Ile | | |
| 305 | 310 | 315 |
| 320 | | |
| Thr Glu Asp Pro Ala Ile Tyr Pro Thr Ala Asp Val Leu Lys Ala Ala | | |
| 325 | 330 | 335 |
| Gln Trp Gln Asp Asp Val Gly Asn Ala Ile Glu Leu Tyr Glu Lys | | |
| 340 | 345 | 350 |

<210> 158

<211> 525

<212> DNA

<213> *Actinobacillus pleuropneumoniae*

<220>

<223> rpmF

<220>

<221> CDS

<222> (1)...(522)

<400> 158

| | |
|---|----|
| atg caa aag gta aaa cta ccc ctc acc att gac cca tat aaa gac gct | 48 |
| Met Gln Lys Val Lys Leu Pro Leu Thr Ile Asp Pro Tyr Lys Asp Ala | |
| 1 | 5 |
| 10 | 15 |

| | |
|---|----|
| cag cgt cga atg gat tac gaa ggc tac atc tca cgt agt ctg ctt aat | 96 |
| Gln Arg Arg Met Asp Tyr Glu Gly Tyr Ile Ser Arg Ser Leu Leu Asn | |
| 20 | 25 |
| 30 | 30 |

| | |
|---|-----|
| cgt ttg ggt gaa tct gtg agc aat gtg cta agc gat gca caa gtt act | 144 |
| Arg Leu Gly Glu Ser Val Ser Asn Val Leu Ser Asp Ala Gln Val Thr | |
| 35 | 40 |
| 45 | 45 |

| | |
|---|-----|
| ctc tcg tta tat atc gat ccg caa cgc tta acc gtt att aaa ggt acg | 192 |
| Leu Ser Leu Tyr Ile Asp Pro Gln Arg Leu Thr Val Ile Lys Gly Thr | |
| 50 | 55 |
| 60 | 60 |

| | |
|---|-----|
| gcg aca gtg gaa gtg gaa ttc gat tgc caa cga tgc ggt aac ccg ttt | 240 |
|---|-----|

| | | | |
|---|-----|-----|-----|
| Ala Thr Val Glu Val Glu Phe Asp Cys Gln Arg Cys Gly Asn Pro Phe | | | |
| 65 | 70 | 75 | 80 |
| aca caa acg ctt gac tgt tcg ttt tgt ttc agt ccg gtg tcc aat atg | 288 | | |
| Thr Gln Thr Leu Asp Cys Ser Phe Cys Phe Ser Pro Val Ser Asn Met | | | |
| 85 | 90 | 95 | |
| gat cag gcg gac aat ttg ccc gaa att tat gaa cca atc gaa gta aac | 336 | | |
| Asp Gln Ala Asp Asn Leu Pro Glu Ile Tyr Glu Pro Ile Glu Val Asn | | | |
| 100 | 105 | 110 | |
| gag ttc ggt gaa gta aat tta cta gat atg atc gaa gat gga ttt atc | 384 | | |
| Glu Phe Gly Glu Val Asn Leu Leu Asp Met Ile Glu Asp Gly Phe Ile | | | |
| 115 | 120 | 125 | |
| atc gaa ttg cct cta gtc ccg atg cat agt gaa gaa cac tgt gaa gtg | 432 | | |
| Ile Glu Leu Pro Leu Val Pro Met His Ser Glu Glu His Cys Glu Val | | | |
| 130 | 135 | 140 | |
| tcc gtg agt gaa cag gtg ttt ggc gaa ttg cct gaa gaa ttg gcg aaa | 480 | | |
| Ser Val Ser Glu Gln Val Phe Gly Glu Leu Pro Glu Glu Leu Ala Lys | | | |
| 145 | 150 | 155 | 160 |
| aaa cct aac ccg ttc gct gta tta gct aat tta aag aaa aac tag | 525 | | |
| Lys Pro Asn Pro Phe Ala Val Ala Asn Leu Lys Lys Asn | | | |
| 165 | 170 | | |

<210> 159

<211> 174

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 159

| | | | |
|---|---|----|----|
| Met Gln Lys Val Lys Leu Pro Leu Thr Ile Asp Pro Tyr Lys Asp Ala | | | |
| 1 | 5 | 10 | 15 |

| | | |
|---|----|----|
| Gln Arg Arg Met Asp Tyr Glu Gly Tyr Ile Ser Arg Ser Leu Leu Asn | | |
| 20 | 25 | 30 |

| | | |
|---|----|----|
| Arg Leu Gly Glu Ser Val Ser Asn Val Leu Ser Asp Ala Gln Val Thr | | |
| 35 | 40 | 45 |

| | | |
|---|----|----|
| Leu Ser Leu Tyr Ile Asp Pro Gln Arg Leu Thr Val Ile Lys Gly Thr | | |
| 50 | 55 | 60 |

| | | | |
|---|----|----|----|
| Ala Thr Val Glu Val Glu Phe Asp Cys Gln Arg Cys Gly Asn Pro Phe | | | |
| 65 | 70 | 75 | 80 |

| | | |
|---|----|----|
| Thr Gln Thr Leu Asp Cys Ser Phe Cys Phe Ser Pro Val Ser Asn Met | | |
| 85 | 90 | 95 |

| | | |
|---|-----|-----|
| Asp Gln Ala Asp Asn Leu Pro Glu Ile Tyr Glu Pro Ile Glu Val Asn | | |
| 100 | 105 | 110 |

| | | |
|---|-----|-----|
| Glu Phe Gly Glu Val Asn Leu Leu Asp Met Ile Glu Asp Gly Phe Ile | | |
| 115 | 120 | 125 |

| | | |
|---|-----|-----|
| Ile Glu Leu Pro Leu Val Pro Met His Ser Glu Glu His Cys Glu Val | | |
| 130 | 135 | 140 |

| | | | |
|---|-----|-----|-----|
| Ser Val Ser Glu Gln Val Phe Gly Glu Leu Pro Glu Glu Leu Ala Lys | | | |
| 145 | 150 | 155 | 160 |

Lys Pro Asn Pro Phe Ala Val Leu Ala Asn Leu Lys Lys Asn
165 170

<210> 160
 <211> 1302
 <212> DNA
 <213> *Actinobacillus pleuropneumoniae*

 <220>
 <223> tig

 <220>
 <221> CDS
 <222> (1) .. (1299)

 <400> 160
 atg tca att tct att gaa act tta gaa ggc tta caa cgc cgc gta act 48
 Met Ser Ile Ser Ile Glu Thr Leu Glu Gly Leu Gln Arg Arg Val Thr
 1 5 10 15

 att acc gta gct gct gat aaa atc gaa ggc gct tac aaa gag caa tta 96
 Ile Thr Val Ala Ala Asp Lys Ile Glu Ala Ala Tyr Lys Glu Gln Leu
 20 25 30

 aaa ggc tat gcg aaa aac gct cgt gta gac ggt ttc cgt aaa ggt aaa 144
 Lys Gly Tyr Ala Lys Asn Ala Arg Val Asp Gly Phe Arg Lys Gly Lys
 35 40 45

 gta ccg cac gca att atc gaa caa cgt ttc ggt tta gcg gct cgc caa 192
 Val Pro His Ala Ile Ile Glu Gln Arg Phe Gly Leu Ala Ala Arg Gln
 50 55 60

 gac gta tta tcc gat gaa atg caa cgt gcg ttc ttt gat gcg gta atc 240
 Asp Val Leu Ser Asp Glu Met Gln Arg Ala Phe Phe Asp Ala Val Ile
 65 70 75 80

 gct gag aaa att aac ctt gcc ggt cgt cct acc ttc aca ccg aac aac 288
 Ala Glu Lys Ile Asn Leu Ala Gly Arg Pro Thr Phe Thr Pro Asn Asn
 85 90 95

 tac caa ccg agt caa gaa ttc agc ttc act gca act ttt gaa gta ttc 336
 Tyr Gln Pro Ser Gln Glu Phe Ser Phe Thr Ala Thr Phe Glu Val Phe
 100 105 110

 ccg gaa gtt gaa tta aaa ggc tta gaa aat atc gaa gtt gaa aaa ccg 384
 Pro Glu Val Glu Leu Lys Gly Leu Glu Asn Ile Glu Val Glu Lys Pro
 115 120 125

 gtt gta gaa atc aca gaa gct gat tta gac aaa atg atc gat gtg tta 432
 Val Val Glu Ile Thr Glu Ala Asp Leu Asp Lys Met Ile Asp Val Leu
 130 135 140

 cgt aaa caa caa gcg act tgg gct gaa tct caa gca gcg gca caa gcg 480
 Arg Lys Gln Gln Ala Thr Trp Ala Glu Ser Gln Ala Ala Ala Gln Ala
 145 150 155 160

 gaa gac cgt gtt gta atc gac ttc gta ggt tct gta gac ggt gaa gag 528
 Glu Asp Arg Val Val Ile Asp Phe Val Gly Ser Val Asp Gly Glu Glu
 165 170 175

 ttt gaa ggc ggt aaa gcg aca gac ttc act tta gca atg ggt caa agt 576
 Phe Glu Gly Gly Lys Ala Thr Asp Phe Thr Leu Ala Met Gly Gln Ser

| 180 | 185 | 190 | |
|--|-----|-----|------|
| cgt atg atc cct ggt ttt gaa gaa ggt atc gtt ggt cac aaa gcc ggc
Arg Met Ile Pro Gly Phe Glu Glu Gly Ile Val Gly His Lys Ala Gly | 195 | 200 | 624 |
| | 205 | | |
| gaa caa ttc gat atc gat gtt act ttc cct gaa gaa tac cac gct gaa
Glu Gln Phe Asp Ile Asp Val Thr Phe Pro Glu Glu Tyr His Ala Glu | 210 | 215 | 672 |
| | 220 | | |
| aac tta aaa ggt aaa gcg gcg aaa ttc gca att aca ctt aag aaa gta
Asn Leu Lys Gly Lys Ala Ala Lys Phe Ala Ile Thr Leu Lys Lys Val | 225 | 230 | 720 |
| | 235 | 240 | |
| gaa aat atc gta tta cct gaa tta acc gaa gaa ttc gtg aaa aaa ttc
Glu Asn Ile Val Leu Pro Glu Leu Thr Glu Glu Phe Val Lys Lys Phe | 245 | 250 | 768 |
| | 255 | | |
| ggt tca gca aaa act gta gaa gat tta cgt gcg gaa att aag aaa aat
Gly Ser Ala Lys Thr Val Glu Asp Leu Arg Ala Glu Ile Lys Lys Asn | 260 | 265 | 816 |
| | 270 | | |
| atg caa cgt gaa ctt aaa aac gca gta acc gca cgc gtt aaa aac caa
Met Gln Arg Glu Leu Lys Asn Ala Val Thr Ala Arg Val Lys Asn Gln | 275 | 280 | 864 |
| | 285 | | |
| gta atc aac ggt tta atc gca caa aat gaa att gaa gtg ccg gct gca
Val Ile Asn Gly Leu Ile Ala Gln Asn Glu Ile Glu Val Pro Ala Ala | 290 | 295 | 912 |
| | 300 | | |
| gcg gta gcg gaa gaa gtg gac gta tta cgt cgt caa gcg gtt caa cgt
Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg | 305 | 310 | 960 |
| | 315 | 320 | |
| tcc ggt ggt aaa ccg gaa atg gct gca caa tta ccg gcg gaa tta ttc
Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe | 325 | 330 | 1008 |
| | 335 | | |
| gaa gcg gat gca aaa cgt cgt gtt caa gta ggt tta tta ctt tca acc
Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Ser Thr | 340 | 345 | 1056 |
| | 350 | | |
| gta atc ggt act aac gaa tta aaa gtt gat gaa aaa cgt gtt gaa gaa
Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu | 355 | 360 | 1104 |
| | 365 | | |
| acg att gca gaa atc gct tca gct tac gaa caa ccg gcg gaa gtt gtt
Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val | 370 | 375 | 1152 |
| | 380 | | |
| gct cat tat gcg aaa aac cgt caa tta acc gaa aat atc cgt aac gta
Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val | 385 | 390 | 1200 |
| | 395 | 400 | |
| gtg tta gaa gag caa gcg gtt gaa gtt gta ctt gcg aaa gca aaa gta
Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val | 405 | 410 | 1248 |
| | 415 | | |
| act gaa aaa gcg act tct ttt gat gaa gta atg gct caa caa gct caa
Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln | 420 | 425 | 1296 |
| | 430 | | |
| ggc taa | | | 1302 |

Gly

<210> 161
<211> 433
<212> PRT
<213> *Actinobacillus pleuropneumoniae*

<400> 161
Met Ser Ile Ser Ile Glu Thr Leu G'l Gly Leu Gln Arg Arg Val Thr
1 5 10 15
Ile Thr Val Ala Ala Asp Lys Ile Glu Ala Ala Tyr Lys Glu Gln Leu
20 25 30
Lys Gly Tyr Ala Lys Asn Ala Arg Val Asp Gly Phe Arg Lys Gly Lys
35 40 45
Val Pro His Ala Ile Ile Glu Gln Arg Phe Gly Leu Ala Ala Arg Gln
50 55 60
Asp Val Leu Ser Asp Glu Met Gln Arg Ala Phe Phe Asp Ala Val Ile
65 70 75 80
Ala Glu Lys Ile Asn Leu Ala Gly Arg Pro Thr Phe Thr Pro Asn Asn
85 90 95
Tyr Gln Pro Ser Gln Glu Phe Ser Phe Thr Ala Thr Phe Glu Val Phe
100 105 110
Pro Glu Val Glu Leu Lys Gly Leu Glu Asn Ile Glu Val Glu Lys Pro
115 120 125
Val Val Glu Ile Thr Glu Ala Asp Leu Asp Lys Met Ile Asp Val Leu
130 135 140
Arg Lys Gln Gln Ala Thr Trp Ala Glu Ser Gln Ala Ala Ala Gln Ala
145 150 155 160
Glu Asp Arg Val Val Ile Asp Phe Val Gly Ser Val Asp Gly Glu Glu
165 170 175
Phe Glu Gly Gly Lys Ala Thr Asp Phe Thr Leu Ala Met Gly Gln Ser
180 185 190
Arg Met Ile Pro Gly Phe Glu Gly Ile Val Gly His Lys Ala Gly
195 200 205
Glu Gln Phe Asp Ile Asp Val Thr Phe Pro Glu Glu Tyr His Ala Glu
210 215 220
Asn Leu Lys Gly Lys Ala Ala Lys Phe Ala Ile Thr Leu Lys Lys Val
225 230 235 240
Glu Asn Ile Val Leu Pro Glu Leu Thr Glu Glu Phe Val Lys Lys Phe
245 250 255
Gly Ser Ala Lys Thr Val Glu Asp Leu Arg Ala Glu Ile Lys Lys Asn
260 265 270
Met Gln Arg Glu Leu Lys Asn Ala Val Thr Ala Arg Val Lys Asn Gln
275 280 285

Val Ile Asn Gly Leu Ile Ala Gln Asn Glu Ile Glu Val Pro Ala Ala
 290 295 300
 Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg
 305 310 315 320
 Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe
 325 330 335
 Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Ser Thr
 340 345 350
 Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu
 355 360 365
 Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val
 370 375 380
 Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val
 385 390 395 400
 Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val
 405 410 415
 Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln
 420 425 430
 Gly

<210> 162
 <211> 316
 <212> DNA
 <213> *Actinobacillus pleuropneumoniae*

 <220>
 <223> tRNA-glu

 <400> 162
 aatattgcgc tcaaatggca aagcggagag catctttaaa tgggttcccc atcgcttaga 60
 ggcctaggac atcgcccttt cacggcgta accggggttc gaatccccgt ggggacgcca 120
 tttaaagatg acttttgttg tctgaattgt tctttaaaaa attggaaaca agctgaaaac 180
 tgagagattt tcgaaagaaa gtctgagtag taaaagataa gtaattatct tgaaaatctt 240
 agctgaacaa aagcagctaa gtgttttagtt gaataaagta tcgcgttgaa tgcgttcaaa 300
 taaaatttga aaatat 316

<210> 163
 <211> 85
 <212> DNA
 <213> *Actinobacillus pleuropneumoniae*

 <220>
 <223> tRNA-leu

 <400> 163
 gctctgggtgg tggaatttgtt agacacgcta tcttgagggg gtagtgtccca taggatgtgc 60

gagttcgagt ctcggccaga gcacc 85

<210> 164
<211> 623
<212> DNA
<213> *Actinobacillus pleuropneumoniae*

<220>
<223> *yaeE*

<220>
<221> CDS
<222> (1)..(621)

<400> 164 48
atg caa gaa ctc aca cct caa atg tgg ggc tta gtc ggc act tca acg
Met Gln Glu Leu Thr Pro Gln Met Trp Gly Leu Val Gly Thr Ser Thr
1 5 10 15

ctt gaa acg ctc tat atg ggc ttt gcg gcg act tta ctt gct gtg gta 96
Leu Glu Thr Leu Tyr Met Gly Phe Ala Ala Thr Leu Leu Ala Val Val
20 25 30

gtc ggt ttg ccg atc ggt ttt ctg gca ttt tta acc ggt aaa gga gag 144
Val Gly Leu Pro Ile Gly Phe Leu Ala Phe Leu Thr Gly Lys Gly Glu
35 40 45

att tta gag aat ccg cgt tta cat caa gta tta gat gtg att att aat 192
Ile Leu Glu Asn Pro Arg Leu His Gln Val Leu Asp Val Ile Ile Asn
50 55 60

atc ggt cgt tcc gta ccg ttt att att ttg tta gtc gtg ttg tta cct 240
Ile Gly Arg Ser Val Pro Phe Ile Ile Leu Leu Val Val Leu Leu Pro
65 70 75 80

ttt acg cgt tta ttg gtc ggg aca acg ctc ggt act acg gcg gcg att 288
Phe Thr Arg Leu Leu Val Gly Thr Thr Leu Gly Thr Thr Ala Ala Ile
85 90 95

gtg ccg tta agc gtt tcg gca att ccg ttt ttt gcg cgt tta act tca 336
Val Pro Leu Ser Val Ser Ala Ile Pro Phe Phe Ala Arg Leu Thr Ser
100 105 110

aat gcg tta tta gaa atc cca gca ggt tta acc gaa gcg gcg aaa tcg 384
Asn Ala Leu Leu Glu Ile Pro Ala Gly Leu Thr Glu Ala Ala Lys Ser
115 120 125

atg ggc gca acg aat tgg caa gtg gtc agt aaa ttt tat tta ccg gaa 432
Met Gly Ala Thr Asn Trp Gln Val Val Ser Lys Phe Tyr Leu Pro Glu
130 135 140

tca ctg ccg att tta atc aat ggt atc aca tta act tta gtc gct tta 480
Ser Leu Pro Ile Leu Ile Asn Gly Ile Thr Leu Thr Leu Val Ala Leu
145 150 155 160

atc ggt tat tcg gca atg gcg ggt gtc ggc ggc ggc ggt ttg ggt 528
Ile Gly Tyr Ser Ala Met Ala Gly Ala Val Gly Gly Gly Gly Leu Gly
165 170 175

aac ctt gcc atc agt tac ggt gaa cac cga aat atg gtc tat gta aaa 576
Asn Leu Ala Ile Ser Tyr Gly Glu His Arg Asn Met Val Tyr Val Lys
180 185 190

| | |
|--|-----|
| tgg atc tca aca att att atc gta gcg att gtg atg atc agt caa aa | 623 |
| Trp Ile Ser Thr Ile Ile Val Ala Ile Val Met Ile Ser Gln | |
| 195 | 200 |
| | 205 |

<210> 165
<211> 207
<212> PRT
<213> *Actinobacillus pleuropneumoniae*

| | |
|---|----|
| <400> 165 | |
| Met Gln Glu Leu Thr Pro Gln Met Trp Gly Leu Val Gly Thr Ser Thr | |
| 1 | 5 |
| | 10 |
| | 15 |

| | |
|---|----|
| Leu Glu Thr Leu Tyr Met Gly Phe Ala Ala Thr Leu Leu Ala Val Val | |
| 20 | 25 |
| | 30 |

| | |
|---|----|
| Val Gly Leu Pro Ile Gly Phe Leu Ala Phe Leu Thr Gly Lys Gly Glu | |
| 35 | 40 |
| | 45 |

| | |
|---|----|
| Ile Leu Glu Asn Pro Arg Leu His Gln Val Leu Asp Val Ile Ile Asn | |
| 50 | 55 |
| | 60 |

| | |
|---|----|
| Ile Gly Arg Ser Val Pro Phe Ile Ile Leu Leu Val Val Leu Leu Pro | |
| 65 | 70 |
| | 75 |
| | 80 |

| | |
|---|----|
| Phe Thr Arg Leu Leu Val Gly Thr Thr Leu Gly Thr Thr Ala Ala Ile | |
| 85 | 90 |
| | 95 |

| | |
|---|-----|
| Val Pro Leu Ser Val Ser Ala Ile Pro Phe Phe Ala Arg Leu Thr Ser | |
| 100 | 105 |
| | 110 |

| | |
|---|-----|
| Asn Ala Leu Leu Glu Ile Pro Ala Gly Leu Thr Glu Ala Ala Lys Ser | |
| 115 | 120 |
| | 125 |

| | |
|---|-----|
| Met Gly Ala Thr Asn Trp Gln Val Val Ser Lys Phe Tyr Leu Pro Glu | |
| 130 | 135 |
| | 140 |

| | |
|---|-----|
| Ser Leu Pro Ile Leu Ile Asn Gly Ile Thr Leu Thr Leu Val Ala Leu | |
| 145 | 150 |
| | 155 |
| | 160 |

| | |
|---|-----|
| Ile Gly Tyr Ser Ala Met Ala Gly Ala Val Gly Gly Gly Gly Leu Gly | |
| 165 | 170 |
| | 175 |

| | |
|---|-----|
| Asn Leu Ala Ile Ser Tyr Gly Glu His Arg Asn Met Val Tyr Val Lys | |
| 180 | 185 |
| | 190 |

| | |
|---|-----|
| Trp Ile Ser Thr Ile Ile Val Ala Ile Val Met Ile Ser Gln | |
| 195 | 200 |
| | 205 |

<210> 166
<211> 866
<212> DNA
<213> *Pasteurella (Mannheimia) haemolytica*

<220>
<221> CDS
<222> (1)...(864)

<220>
<223> atpG

<400> 166
atg gca ggt gct aaa gag ata aga acc aaa att gca agt gtt cgt aat 48
Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Arg Asn
1 5 10 15

aca caa aaa att acc aaa gcg atg gaa atg gtt gcc gca tca aaa atg 96
Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys Met
20 25 30

cgt aaa acc caa gag cgt atg gcg gct tct cgc cct tat gct gaa agt 144
Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ala Glu Ser
35 40 45

att cgc aag gca att agc cat att gcc aaa ggt aac att gag tat aaa 192
Ile Arg Lys Ala Ile Ser His Ile Ala Lys Gly Asn Ile Glu Tyr Lys
50 55 60

cac cca ttt ttg acc cca cgt ccg gta aaa aaa gtt ggc tat tta gta 240
His Pro Phe Leu Thr Pro Arg Pro Val Lys Lys Val Gly Tyr Leu Val
65 70 75 80

gtt tca acc gat cgc ggt tta tgt ggt ggc tta aat atc aat tta ttt 288
Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe
85 90 95

aaa acc gtt tta cat gaa ttg aaa gaa aaa gat gac caa ggt gtt aag 336
Lys Thr Val Leu His Glu Leu Lys Glu Lys Asp Asp Gln Gly Val Lys
100 105 110

tct cga ctt gct gtg gtg gga aat aaa ggg atc tcc ttt ttt aac cca 384
Ser Arg Leu Ala Val Val Gly Asn Lys Gly Ile Ser Phe Phe Asn Pro
115 120 125

atg ggg cta gag att aaa ggt cat atc aat gga ttg ggt gat aca ccg 432
Met Gly Leu Glu Ile Lys Gly His Ile Asn Gly Leu Gly Asp Thr Pro
130 135 140

gca atg gaa gat tta gtc ggt att gtt aat ggt atg gta aat gcc tac 480
Ala Met Glu Asp Leu Val Gly Ile Val Asn Gly Met Val Asn Ala Tyr
145 150 155 160

cgt gaa ggc gaa att gat gaa gtg tat gtg gta tat aac cgt ttt ata 528
Arg Glu Gly Glu Ile Asp Glu Val Tyr Val Val Tyr Asn Arg Phe Ile
165 170 175

aac acg atg tca caa aaa ccg aca gta caa cag ttg ctt cct ttg cct 576
Asn Thr Met Ser Gln Lys Pro Thr Val Gln Gln Leu Leu Pro Leu Pro
180 185 190

gca ctg gaa aat gac tca tta gag caa act ggt tct tgg gat tat ctc 624
Ala Leu Glu Asn Asp Ser Leu Glu Gln Thr Gly Ser Trp Asp Tyr Leu
195 200 205

tat gaa cca aat cca caa gcg tta tta gac agc tta ctg gtt cgt tat 672
Tyr Glu Pro Asn Pro Gln Ala Leu Leu Asp Ser Leu Leu Val Arg Tyr
210 215 220

tta gaa tct caa gtt tat cag gca gtg gta gat aat ctt gcg tct gaa 720
Leu Glu Ser Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu
225 230 235 240

cag gct gct cga atg gtg gca atg aaa gca gca acc gat aac gca ggt 768
Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly

Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly
 245 250 255

Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala
 260 265 270

Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile
 275 280 285

<210> 168

<211> 1463

<212> DNA

<213> Pasteurella (Mannheimia) haemolytica

<220>

<221> CDS

<222> (1)..(1461)

<220>

<223> guaB

<400> 168

| | |
|---|----|
| atg cta cga att aaa caa gaa gcc ctc act ttt gat gat gtt ctt ctc | 48 |
| Met Leu Arg Ile Lys Gln Glu Ala Leu Thr Phe Asp Asp Val Leu Leu | |
| 1 5 10 15 | |

| | |
|---|----|
| gtc ccg gca cat tct act gtg ctt cct aat act gct gat ctt tct act | 96 |
| Val Pro Ala His Ser Thr Val Leu Pro Asn Thr Ala Asp Leu Ser Thr | |
| 20 25 30 | |

| | |
|---|-----|
| caa tta act aaa acc att cgt tta aac att ccg atg ctt tct gct gca | 144 |
| Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro Met Leu Ser Ala Ala | |
| 35 40 45 | |

| | |
|---|-----|
| atg gat acc gtt aca gaa act aag ctt gcg atc tcc ctt gct caa gaa | 192 |
| Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile Ser Leu Ala Gln Glu | |
| 50 55 60 | |

| | |
|---|-----|
| ggc ggc att ggt ttt atc cat aaa aat atg tcg att gaa cgc cag gca | 240 |
| Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser Ile Glu Arg Gln Ala | |
| 65 70 75 80 | |

| | |
|---|-----|
| gac cgt gtg cgt aaa gtg aaa aaa ttt gaa agt ggt att gtt tct gag | 288 |
| Asp Arg Val Arg Lys Val Lys Lys Phe Glu Ser Gly Ile Val Ser Glu | |
| 85 90 95 | |

| | |
|---|-----|
| cca gtg acg att tct cct gat atg aca tta gcg gaa ttg gct gaa ttg | 336 |
| Pro Val Thr Ile Ser Pro Asp Met Thr Leu Ala Glu Leu Ala Glu Leu | |
| 100 105 110 | |

| | |
|---|-----|
| gtg aaa aag aac ggt ttt gca ggc tat ccg gtg att gat gaa aac caa | 384 |
| Val Lys Lys Asn Gly Phe Ala Gly Tyr Pro Val Ile Asp Glu Asn Gln | |
| 115 120 125 | |

| | |
|---|-----|
| aat tta gtg gga att att acc gga cgt gat acc cga ttt gtc acg gat | 432 |
| Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr Arg Phe Val Thr Asp | |
| 130 135 140 | |

| | |
|---|-----|
| tta agc aaa aca gtg cgt gaa ttt atg aca cca aaa gac cgt tta gtg | 480 |
| Leu Ser Lys Thr Val Arg Glu Phe Met Thr Pro Lys Asp Arg Leu Val | |
| 145 150 155 160 | |

| | |
|---|------|
| acg gta aaa gaa aac gca agc cgt gaa gaa att ttc cac tta atg cac | 528 |
| Thr Val Lys Glu Asn Ala Ser Arg Glu Glu Ile Phe His Leu Met His | |
| 165 | 170 |
| | 175 |
| gaa cac cga gtg gag aaa gtg ctg gta gtg aat aat gaa ttt cag tta | 576 |
| Glu His Arg Val Glu Lys Val Leu Val Val Asn Asn Glu Phe Gln Leu | |
| 180 | 185 |
| | 190 |
| aaa gga atg att acc cta aaa gac tac caa aaa gcg gaa agc aaa ccg | 624 |
| Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys Ala Glu Ser Lys Pro | |
| 195 | 200 |
| | 205 |
| aat gcc tgt aaa gat gag ttt ggg cgt ttg cgt gtg ggg gcg gca gtg | 672 |
| Asn Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg Val Gly Ala Ala Val | |
| 210 | 215 |
| | 220 |
| gga gcc ggt ccg ggc aat gaa gaa cga att gat gct tta gta aaa gcg | 720 |
| Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp Ala Leu Val Lys Ala | |
| 225 | 230 |
| | 235 |
| | 240 |
| ggg gtc gat gtg cta tta atc gac tct tcg cac ggg cat tct gaa ggt | 768 |
| Gly Val Asp Val Leu Leu Ile Asp Ser Ser His Gly His Ser Glu Gly | |
| 245 | 250 |
| | 255 |
| gta tta caa cgt gtg cgt gaa acc cgt gca aaa tac cct gat tta ccg | 816 |
| Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys Tyr Pro Asp Leu Pro | |
| 260 | 265 |
| | 270 |
| att gtt gcc ggt aat att gcc act gca gaa gga gcg att gcg tta gct | 864 |
| Ile Val Ala Gly Asn Ile Ala Thr Ala Glu Gly Ala Ile Ala Leu Ala | |
| 275 | 280 |
| | 285 |
| gat gca gga gcc agt gct gtg aaa gta gga atc ggc ccg ggt tca att | 912 |
| Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile Gly Pro Gly Ser Ile | |
| 290 | 295 |
| | 300 |
| tgt acc acc aga att gta aca ggc gtt ggc gtg cca caa atc acg gca | 960 |
| Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val Pro Gln Ile Thr Ala | |
| 305 | 310 |
| | 315 |
| | 320 |
| atc gca gaa gcg gca gct gcg ctt aaa gaa cga ggc att cct gtg att | 1008 |
| Ile Ala Glu Ala Ala Ala Leu Lys Glu Arg Gly Ile Pro Val Ile | |
| 325 | 330 |
| | 335 |
| gct gat ggt gga att cgt tat tca ggc gat att tca aaa gct att gcc | 1056 |
| Ala Asp Gly Gly Ile Arg Tyr Ser Gly Asp Ile Ser Lys Ala Ile Ala | |
| 340 | 345 |
| | 350 |
| gcc ggt gca agt tgc gta atg gtc ggt tcg atg ttt gcc ggc aca gaa | 1104 |
| Ala Gly Ala Ser Cys Val Met Val Gly Ser Met Phe Ala Gly Thr Glu | |
| 355 | 360 |
| | 365 |
| gaa gcc ccg ggt gaa att gag ctt tat caa ggc aga gca ttc aaa tcc | 1152 |
| Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly Arg Ala Phe Lys Ser | |
| 370 | 375 |
| | 380 |
| tac cgt gga atg gga tca tta ggt gca atg agt aaa ggc tcg tca gat | 1200 |
| Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser Lys Gly Ser Ser Asp | |
| 385 | 390 |
| | 395 |
| | 400 |
| cgc tat ttc caa tct gat aat gcc gcc gac aag ctc gta ccg gaa ggg | 1248 |
| Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys Leu Val Pro Glu Gly | |
| 405 | 410 |
| | 415 |

| | |
|---|------|
| att gaa ggg cgt atc gct tac aaa ggc tac ttg aaa gaa att atc cac | 1296 |
| Ile Glu Gly Arg Ile Ala Tyr Lys Gly Tyr Leu Lys Glu Ile Ile His | |
| 420 | 425 |
| 430 | |
| caa caa atg ggc ggc tta cgc tcc tgt atg gga tta acc ggc tgt gcc | 1344 |
| Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly Leu Thr Gly Cys Ala | |
| 435 | 440 |
| 445 | |
| act att gaa gaa ctc cgc acc aaa gca gaa ttt gtc cgc att agt ggt | 1392 |
| Thr Ile Glu Glu Leu Arg Thr Lys Ala Glu Phe Val Arg Ile Ser Gly | |
| 450 | 455 |
| 460 | |
| gct ggt att aaa gaa agc cac gtc cac gat gtg aca att acc aaa gaa | 1440 |
| Ala Gly Ile Lys Glu Ser His Val His Asp Val Thr Ile Thr Lys Glu | |
| 465 | 470 |
| 475 | |
| 480 | |
| gca ccg aac tac cga atg ggt ta | 1463 |
| Ala Pro Asn Tyr Arg Met Gly | |
| 485 | |

<210> 169

<211> 487

<212> PRT

<213> Pasteurella (Mannheimia) haemolytica

<400> 169

| | |
|---|---|
| Met Leu Arg Ile Lys Gln Glu Ala Leu Thr Phe Asp Asp Val Leu Leu | |
| 1 | 5 |
| 10 | |
| 15 | |

| | |
|---|----|
| Val Pro Ala His Ser Thr Val Leu Pro Asn Thr Ala Asp Leu Ser Thr | |
| 20 | 25 |
| 30 | |

| | |
|---|----|
| Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro Met Leu Ser Ala Ala | |
| 35 | 40 |
| 45 | |

| | |
|---|----|
| Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile Ser Leu Ala Gln Glu | |
| 50 | 55 |
| 60 | |

| | |
|---|----|
| Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser Ile Glu Arg Gln Ala | |
| 65 | 70 |
| 75 | |
| 80 | |

| | |
|---|----|
| Asp Arg Val Arg Lys Val Lys Lys Phe Glu Ser Gly Ile Val Ser Glu | |
| 85 | 90 |
| 95 | |

| | |
|---|-----|
| Pro Val Thr Ile Ser Pro Asp Met Thr Leu Ala Glu Leu Ala Glu Leu | |
| 100 | 105 |
| 110 | |

| | |
|---|-----|
| Val Lys Lys Asn Gly Phe Ala Gly Tyr Pro Val Ile Asp Glu Asn Gln | |
| 115 | 120 |
| 125 | |

| | |
|---|-----|
| Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr Arg Phe Val Thr Asp | |
| 130 | 135 |
| 140 | |

| | |
|---|-----|
| Leu Ser Lys Thr Val Arg Glu Phe Met Thr Pro Lys Asp Arg Leu Val | |
| 145 | 150 |
| 155 | |
| 160 | |

| | |
|---|-----|
| Thr Val Lys Glu Asn Ala Ser Arg Glu Glu Ile Phe His Leu Met His | |
| 165 | 170 |
| 175 | |

| | |
|---|-----|
| Glu His Arg Val Glu Lys Val Leu Val Val Asn Asn Glu Phe Gln Leu | |
| 180 | 185 |
| 190 | |

Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys Ala Glu Ser Lys Pro
 195 200 205
 Asn Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg Val Gly Ala Ala Val
 210 215 220
 Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp Ala Leu Val Lys Ala
 225 230 235 240
 Gly Val Asp Val Leu Leu Ile Asp Ser Ser His Gly His Ser Glu Gly
 245 250 255
 Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys Tyr Pro Asp Leu Pro
 260 265 270
 Ile Val Ala Gly Asn Ile Ala Thr Ala Glu Gly Ala Ile Ala Leu Ala
 275 280 285
 Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile Gly Pro Gly Ser Ile
 290 295 300
 Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val Pro Gln Ile Thr Ala
 305 310 315 320
 Ile Ala Glu Ala Ala Ala Leu Lys Glu Arg Gly Ile Pro Val Ile
 325 330 335
 Ala Asp Gly Gly Ile Arg Tyr Ser Gly Asp Ile Ser Lys Ala Ile Ala
 340 345 350
 Ala Gly Ala Ser Cys Val Met Val Gly Ser Met Phe Ala Gly Thr Glu
 355 360 365
 Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly Arg Ala Phe Lys Ser
 370 375 380
 Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser Lys Gly Ser Ser Asp
 385 390 395 400
 Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys Leu Val Pro Glu Gly
 405 410 415
 Ile Glu Gly Arg Ile Ala Tyr Lys Gly Tyr Leu Lys Glu Ile Ile His
 420 425 430
 Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly Leu Thr Gly Cys Ala
 435 440 445
 Thr Ile Glu Glu Leu Arg Thr Lys Ala Glu Phe Val Arg Ile Ser Gly
 450 455 460
 Ala Gly Ile Lys Glu Ser His Val His Asp Val Thr Ile Thr Lys Glu
 465 470 475 480
 Ala Pro Asn Tyr Arg Met Gly
 485

<210> 170
 <211> 2150
 <212> DNA
 <213> Pasteurella (Mannheimia) haemolytica

<220>
 <221> CDS
 <222> (1)...(2148)

<220>
 <223> pnp

<400> 170

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|---|----|
| atg act cca att gta aaa cag ttt aaa tac ggt cag cac acc gtg acc | 48 |
| Met Thr Pro Ile Val Lys Gln Phe Lys Tyr Gly Gln His Thr Val Thr | |
| 1 | 5 |
| 10 | 15 |

tta gaa acc ggt gct atc gca cgc caa gca acg gca gca gta atg gca

| | |
|---|----|
| Leu Glu Thr Gly Ala Ile Ala Arg Gln Ala Thr Ala Ala Val Met Ala | 96 |
| 20 | 25 |
| 30 | |

agt atg gac gac aca acc gta ttt gtt acc gta gta gcg aaa aaa gac

| | |
|---|-----|
| Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys Lys Asp | 144 |
| 35 | 40 |
| 45 | |

gta aaa gaa ggg caa gat ttc ttc cca tta acc gta gat tat caa gag

| | |
|---|-----|
| Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asp Tyr Gln Glu | 192 |
| 50 | 55 |
| 60 | |

cgt act tac gca gcc ggt cgt att ccg ggc ggt ttc ttc aaa cgt gaa

| | |
|---|-----|
| Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Gly Phe Phe Lys Arg Glu | 240 |
| 65 | 70 |
| 75 | 80 |

gga cgt cct agc gaa ggt gaa acc tta atc gct cgc ttg atc gac cgt

| | |
|---|-----|
| Gly Arg Pro Ser Glu Gly Glu Thr Leu Ile Ala Arg Leu Ile Asp Arg | 288 |
| 85 | 90 |
| 95 | |

cct gtg cgt cca ctt ttc cca gaa ggt ttc ttt aac gaa att caa gtg

| | |
|---|-----|
| Pro Val Arg Pro Leu Phe Pro Glu Gly Phe Phe Asn Glu Ile Gln Val | 336 |
| 100 | 105 |
| 110 | |

att gcg acc gta gta tcg gta aac cca caa atc agt cct gat ctg gtt

| | |
|---|-----|
| Ile Ala Thr Val Val Ser Val Asn Pro Gln Ile Ser Pro Asp Leu Val | 384 |
| 115 | 120 |
| 125 | |

gcg atg atc ggt gca tcg gct gcc ctt tca tta tcc ggc gtg ccg ttt

| | |
|---|-----|
| Ala Met Ile Gly Ala Ser Ala Ala Leu Ser Leu Ser Gly Val Pro Phe | 432 |
| 130 | 135 |
| 140 | |

aac ggt cca atc ggt gcg gct cgt gtc ggt ttt atc aac gat caa ttc

| | |
|---|-----|
| Asn Gly Pro Ile Gly Ala Ala Arg Val Gly Phe Ile Asn Asp Gln Phe | 480 |
| 145 | 150 |
| 155 | 160 |

gta tta aac cca acc acc agc gag caa aaa atc agc cgc tta gat tta

| | |
|---|-----|
| Val Leu Asn Pro Thr Thr Ser Glu Gln Lys Ile Ser Arg Leu Asp Leu | 528 |
| 165 | 170 |
| 175 | |

gtg gtt tca ggt aca gac aaa gcc gtg ttg atg gtg gaa tct gaa gcg

| | |
|---|-----|
| Val Val Ser Gly Thr Asp Lys Ala Val Leu Met Val Glu Ser Glu Ala | 576 |
| 180 | 185 |
| 190 | |

gat atc tta acc gaa gag caa atg tta gcg gcg gtg gtg ttc ggc cac

| | |
|---|-----|
| Asp Ile Leu Thr Glu Glu Gln Met Leu Ala Ala Val Val Phe Gly His | 624 |
| 195 | 200 |
| 205 | |

gag caa caa cag gtt gta atc gaa aac atc aaa gaa ttt gtt aaa gaa

| | |
|---|-----|
| Glu Gln Gln Gln Val Val Ile Glu Asn Ile Lys Glu Phe Val Lys Glu | 672 |
| 210 | 215 |
| 220 | |

| | |
|---|------|
| gcg ggc aaa cca cgt tgg gat tgg gtt gca cca gag cca aat aca gat
Ala Gly Lys Pro Arg Trp Asp Trp Val Ala Pro Glu Pro Asn Thr Asp
225 230 235 240 | 720 |
| tta atc aac aaa gta aaa gca tta gca gaa aca cgc ctt ggc gat gct
Leu Ile Asn Lys Val Lys Ala Leu Ala Glu Thr Arg Leu Gly Asp Ala
245 250 255 | 768 |
| tat cgt atc gta gaa aaa caa gtt cgt tac gag caa atc gat gcg att
Tyr Arg Ile Val Glu Lys Gln Val Arg Tyr Glu Gln Ile Asp Ala Ile
260 265 270 | 816 |
| aaa gca gag gtg att gca caa ctt acc gca gaa gat gaa act gtt tct
Lys Ala Glu Val Ile Ala Gln Leu Thr Ala Glu Asp Glu Thr Val Ser
275 280 285 | 864 |
| gaa ggg act atc atc gac atc acc gca tta gag agc caa atc gtg
Glu Gly Thr Ile Ile Asp Ile Ile Thr Ala Leu Glu Ser Gln Ile Val
290 295 300 | 912 |
| cgt agc cgt att att gca ggc gaa cca cgc att gac ggc cgt acg gtg
Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr Val
305 310 315 320 | 960 |
| gat acc gtg cgt gca ttg gat att tgc acc agt gtg tta cca cgc acc
Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Ser Val Leu Pro Arg Thr
325 330 335 | 1008 |
| cac ggt tct gct ctt ttc acc cgt ggc gaa acc caa gca tta gca gta
His Gly Ser Ala Leu Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala Val
340 345 350 | 1056 |
| gca aca ttg ggc aca gag cgt gat gcc caa atc att gac gaa ttg acc
Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu Thr
355 360 365 | 1104 |
| ggc gaa aaa tct gac cgt ttc tta ttc cac tac aat ttc cct cca tac
Gly Glu Lys Ser Asp Arg Phe Leu Phe His Tyr Asn Phe Pro Pro Tyr
370 375 380 | 1152 |
| tct gtg ggc gaa acc ggt cgt atc ggc tcg cca aaa cgc cgt gaa atc
Ser Val Gly Glu Thr Gly Arg Ile Gly Ser Pro Lys Arg Arg Glu Ile
385 390 395 400 | 1200 |
| ggt cac ggt cgt tta gca aaa cgt ggc gta tta gcc gtg atg cca acc
Gly His Gly Arg Leu Ala Lys Arg Gly Val Leu Ala Val Met Pro Thr
405 410 415 | 1248 |
| gct gaa gag ttc ccg tat gta gtg cgt gtg gtg tct gaa atc act gaa
Ala Glu Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr Glu
420 425 430 | 1296 |
| tct aac ggt tct tca atg gca tct gtg tgt ggt gcg tct ctt gcg
Ser Asn Gly Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu Ala
435 440 445 | 1344 |
| ttg atg gac gca ggt gtg cca atc aaa gca gcg gtt gcc ggt atc gca
Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile Ala
450 455 460 | 1392 |
| atg ggg ctc gtg aaa gaa gac gag aaa ttc gtg gta ctt tct gac atc
Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp Ile
465 470 475 480 | 1440 |

| | |
|---|------|
| tta ggt gat gaa gac cac tta ggc gat atg gac ttt aaa gta gcg gga | 1488 |
| Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala Gly | |
| 485 | 490 |
| 495 | |
| acc cgt acc ggt gtg act gcg ctg caa atg gac atc aaa atc gaa ggg | 1536 |
| Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu Gly | |
| 500 | 505 |
| 510 | |
| atc acc cct gaa att atg cgt att gcc tta aac caa gct aaa ggt gca | 1584 |
| Ile Thr Pro Glu Ile Met Arg Ile Ala Leu Asn Gln Ala Lys Gly Ala | |
| 515 | 520 |
| 525 | |
| aga atg cac att tta ggt gta atg gaa caa gcc att ccg gca cct cgt | 1632 |
| Arg Met His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro Arg | |
| 530 | 535 |
| 540 | |
| gca gat att tct gac tat gcc cca cgc att cac aca atg aag atc gat | 1680 |
| Ala Asp Ile Ser Asp Tyr Ala Pro Arg Ile His Thr Met Lys Ile Asp | |
| 545 | 550 |
| 555 | 560 |
| ccg aag aaa atc aaa gat gtg att ggt aaa ggc ggt gca aca att cgt | 1728 |
| Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile Arg | |
| 565 | 570 |
| 575 | |
| gct tta acc gaa gag acc aat act tct atc gac att gat gat gac ggt | 1776 |
| Ala Leu Thr Glu Glu Thr Asn Thr Ser Ile Asp Ile Asp Asp Asp Gly | |
| 580 | 585 |
| 590 | |
| acg gtg aaa att gcg gca act gac ggc aat gca gcg aaa gca gta atg | 1824 |
| Thr Val Lys Ile Ala Ala Thr Asp Gly Asn Ala Ala Lys Ala Val Met | |
| 595 | 600 |
| 605 | |
| gct cgt att gaa gag atc gtt gcc gaa gtg gaa gta aac caa atc tac | 1872 |
| Ala Arg Ile Glu Glu Ile Val Ala Glu Val Glu Val Asn Gln Ile Tyr | |
| 610 | 615 |
| 620 | |
| aac ggt aaa gta acc cgt gtg gtc gac ttc ggt gca ttc gtt tcc atc | 1920 |
| Asn Gly Lys Val Thr Arg Val Val Asp Phe Gly Ala Phe Val Ser Ile | |
| 625 | 630 |
| 635 | 640 |
| tta ggt ggc aaa gaa ggt tta gtc cac att tca caa atc acc aac gaa | 1968 |
| Leu Gly Gly Lys Glu Gly Leu Val His Ile Ser Gln Ile Thr Asn Glu | |
| 645 | 650 |
| 655 | |
| cgt gtt gag cgt gta gcg gac tac tta acc gtt ggt caa gaa gta caa | 2016 |
| Arg Val Glu Arg Val Ala Asp Tyr Leu Thr Val Gly Gln Glu Val Gln | |
| 660 | 665 |
| 670 | |
| gtg aaa gtg gta gaa att gac cgt caa gga cgc att cgt ctg acg atg | 2064 |
| Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr Met | |
| 675 | 680 |
| 685 | |
| aaa gac atc aat aat acc aac gag gca aat gca gaa gaa act gta gct | 2112 |
| Lys Asp Ile Asn Asn Thr Asn Glu Ala Asn Ala Glu Glu Thr Val Ala | |
| 690 | 695 |
| 700 | |
| gaa aat gtg gta gaa aca gaa caa gaa aat aat ttc ta | 2150 |
| Glu Asn Val Val Glu Thr Glu Gln Glu Asn Asn Phe | |
| 705 | 710 |
| 715 | |

<210> 171
<211> 716

<212> PRT

<213> Pasteurella (Mannheimia) haemolytica

<400> 171

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Pro | Ile | Val | Lys | Gln | Phe | Lys | Tyr | Gly | Gln | His | Thr | Val | Thr |
| 1 | | | | | | | | | | | | | | | 15 |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Glu | Thr | Gly | Ala | Ile | Ala | Arg | Gln | Ala | Thr | Ala | Ala | Val | Met | Ala |
| | | | | 20 | | | | 25 | | | | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ser | Met | Asp | Asp | Thr | Thr | Val | Phe | Val | Thr | Val | Val | Ala | Lys | Lys | Asp |
| | | | | 35 | | | | 40 | | | | 45 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Lys | Glu | Gly | Gln | Asp | Phe | Phe | Pro | Leu | Thr | Val | Asp | Tyr | Gln | Glu |
| | | | | 50 | | | | | 55 | | | 60 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Thr | Tyr | Ala | Ala | Gly | Arg | Ile | Pro | Gly | Gly | Phe | Phe | Lys | Arg | Glu |
| 65 | | | | | 70 | | | | 75 | | | | 80 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Gly | Arg | Pro | Ser | Glu | Gly | Glu | Thr | Leu | Ile | Ala | Arg | Leu | Ile | Asp | Arg |
| | | | | 85 | | | | 90 | | | 95 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Val | Arg | Pro | Leu | Phe | Pro | Glu | Gly | Phe | Phe | Asn | Glu | Ile | Gln | Val |
| | | | | 100 | | | | 105 | | | 110 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ile | Ala | Thr | Val | Val | Ser | Val | Asn | Pro | Gln | Ile | Ser | Pro | Asp | Leu | Val |
| | | | | | 115 | | | 120 | | | 125 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Met | Ile | Gly | Ala | Ser | Ala | Ala | Leu | Ser | Leu | Ser | Gly | Val | Pro | Phe |
| | | | | 130 | | | | 135 | | | 140 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Gly | Pro | Ile | Gly | Ala | Ala | Arg | Val | Gly | Phe | Ile | Asn | Asp | Gln | Phe |
| 145 | | | | | 150 | | | | 155 | | | 160 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Leu | Asn | Pro | Thr | Thr | Ser | Glu | Gln | Lys | Ile | Ser | Arg | Leu | Asp | Leu |
| | | | | | 165 | | | | 170 | | | 175 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Val | Ser | Gly | Thr | Asp | Lys | Ala | Val | Leu | Met | Val | Glu | Ser | Glu | Ala |
| | | | | | 180 | | | | 185 | | | 190 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asp | Ile | Leu | Thr | Glu | Glu | Gln | Met | Leu | Ala | Ala | Val | Val | Phe | Gly | His |
| | | | | | 195 | | | 200 | | | 205 | | | | |

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Gln | Gln | Val | Val | Ile | Glu | Asn | Ile | Lys | Glu | Phe | Val | Lys | Glu |
| | | | | | 210 | | | 215 | | | 220 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Gly | Lys | Pro | Arg | Trp | Asp | Trp | Val | Ala | Pro | Glu | Pro | Asn | Thr | Asp |
| 225 | | | | | 230 | | | | 235 | | | 240 | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ile | Asn | Lys | Val | Lys | Ala | Leu | Ala | Glu | Thr | Arg | Leu | Gly | Asp | Ala |
| | | | | | 245 | | | 250 | | | 255 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Tyr | Arg | Ile | Val | Glu | Lys | Gln | Val | Arg | Tyr | Glu | Gln | Ile | Asp | Ala | Ile |
| | | | | | 260 | | | 265 | | | 270 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Ala | Glu | Val | Ile | Ala | Gln | Leu | Thr | Ala | Glu | Asp | Glu | Thr | Val | Ser |
| | | | | | 275 | | | 280 | | | 285 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Gly | Thr | Ile | Ile | Asp | Ile | Ile | Thr | Ala | Leu | Glu | Ser | Gln | Ile | Val |
| | | | | | 290 | | | 295 | | | 300 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Ser | Arg | Ile | Ile | Ala | Gly | Glu | Pro | Arg | Ile | Asp | Gly | Arg | Thr | Val |
| 305 | | | | | 310 | | | | 315 | | | 320 | | | |

Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Ser Val Leu Pro Arg Thr
 325 330 335
 His Gly Ser Ala Leu Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala Val
 340 345 350
 Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu Thr
 355 360 365
 Gly Glu Lys Ser Asp Arg Phe Leu Phe His Tyr Asn Phe Pro Pro Tyr
 370 375 380
 Ser Val Gly Glu Thr Gly Arg Ile Gly Ser Pro Lys Arg Arg Glu Ile
 385 390 395 400
 Gly His Gly Arg Leu Ala Lys Arg Gly Val Leu Ala Val Met Pro Thr
 405 410 415
 Ala Glu Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr Glu
 420 425 430
 Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu Ala
 435 440 445
 Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile Ala
 450 455 460
 Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp Ile
 465 470 475 480
 Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala Gly
 485 490 495
 Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu Gly
 500 505 510
 Ile Thr Pro Glu Ile Met Arg Ile Ala Leu Asn Gln Ala Lys Gly Ala
 515 520 525
 Arg Met His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro Arg
 530 535 540
 Ala Asp Ile Ser Asp Tyr Ala Pro Arg Ile His Thr Met Lys Ile Asp
 545 550 555 560
 Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile Arg
 565 570 575
 Ala Leu Thr Glu Glu Thr Asn Thr Ser Ile Asp Ile Asp Asp Asp Gly
 580 585 590
 Thr Val Lys Ile Ala Ala Thr Asp Gly Asn Ala Ala Lys Ala Val Met
 595 600 605
 Ala Arg Ile Glu Glu Ile Val Ala Glu Val Glu Val Asn Gln Ile Tyr
 610 615 620
 Asn Gly Lys Val Thr Arg Val Val Asp Phe Gly Ala Phe Val Ser Ile
 625 630 635 640
 Leu Gly Gly Lys Glu Gly Leu Val His Ile Ser Gln Ile Thr Asn Glu
 645 650 655

Arg Val Glu Arg Val Ala Asp Tyr Leu Thr Val Gly Gln Glu Val Gln
 660 665 670

Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr Met
 675 680 685

Lys Asp Ile Asn Asn Thr Asn Glu Ala Asn Ala Glu Glu Thr Val Ala
 690 695 700

Glu Asn Val Val Glu Thr Glu Gln Glu Asn Asn Phe
 705 710 715

<210> 172

<211> 1517

<212> DNA

<213> Pasteurella (Mannheimia) haemolytica

<220>

<221> CDS

<222> (1)...(1515)

<220>

<223> purF

<400> 172

| | |
|---|----|
| atg tgc ggc att gtc ggt att att ggg aat tcg ccg gtg aat cag gcg | 48 |
| Met Cys Gly Ile Val Gly Ile Ile Gly Asn Ser Pro Val Asn Gln Ala | |
| 1 5 10 15 | |

| | |
|---|----|
| att tat gat ggt tta aca tta ctt caa cac cga gga caa gat gcc gca | 96 |
| Ile Tyr Asp Gly Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala | |
| 20 25 30 | |

| | |
|---|-----|
| ggt atc gtc acc ata gac gat gaa aat cgt ttc cgc tta cgc aaa gct | 144 |
| Gly Ile Val Thr Ile Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala | |
| 35 40 45 | |

| | |
|---|-----|
| aac ggc tta gtc agc gat gtt ttc cag caa gag cat atg gtg aga tta | 192 |
| Asn Gly Leu Val Ser Asp Val Phe Gln Gln Glu His Met Val Arg Leu | |
| 50 55 60 | |

| | |
|---|-----|
| caa ggc aat gtt gga att ggt cac gtt cgc tac cca aca gca ggt agc | 240 |
| Gln Gly Asn Val Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser | |
| 65 70 75 80 | |

| | |
|---|-----|
| tca agt gtg tct gaa gcc cag cca ttt tat gtc aat tca cct ttc ggt | 288 |
| Ser Ser Val Ser Ala Gln Pro Phe Tyr Val Asn Ser Pro Phe Gly | |
| 85 90 95 | |

| | |
|---|-----|
| att acc tta gtt cac aac ggt aat tta act aat aat gcg gaa ctt aaa | 336 |
| Ile Thr Leu Val His Asn Gly Asn Leu Thr Asn Asn Ala Glu Leu Lys | |
| 100 105 110 | |

| | |
|---|-----|
| gct cgc tta tac aac gaa gcc cgc cgc cat gtg aac act aat tct gat | 384 |
| Ala Arg Leu Tyr Asn Glu Ala Arg Arg His Val Asn Thr Asn Ser Asp | |
| 115 120 125 | |

| | |
|---|-----|
| tct gaa tcc ctt ctt aat att ttt gct tac ttt tta gat ctc tat tcc | 432 |
| Ser Glu Ser Leu Leu Asn Ile Phe Ala Tyr Phe Leu Asp Leu Tyr Ser | |
| 130 135 140 | |

| | |
|---|-----|
| act cag cat tta agc cca gac aat atc ttt gaa acg gtt cgt aaa acc | 480 |
|---|-----|

| | | | | |
|---|------|-----|-----|--|
| Thr Gln His Leu Ser Pro Asp Asn Ile Phe Glu Thr Val Arg Lys Thr | | | | |
| 145 | 150 | 155 | 160 | |
| aat gat agc att cgt ggt gct tat gct tgc att gcg atg att atc gga | 528 | | | |
| Asn Asp Ser Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly | | | | |
| 165 | 170 | 175 | | |
| cac ggt atg gtt gct ttc cgt gac cca ttc ggt att cgc ccg tta gtg | 576 | | | |
| His Gly Met Val Ala Phe Arg Asp Pro Phe Gly Ile Arg Pro Leu Val | | | | |
| 180 | 185 | 190 | | |
| ctg ggt aaa cgt gaa atc gag ggt aaa acc gaa tat atg ttt gct tcg | 624 | | | |
| Leu Gly Lys Arg Glu Ile Glu Gly Lys Thr Glu Tyr Met Phe Ala Ser | | | | |
| 195 | 200 | 205 | | |
| gaa agt gtg gct ctt gat gta gtg ggg ttt gaa ttt gtg cga gat gtg | 672 | | | |
| Glu Ser Val Ala Leu Asp Val Val Gly Phe Glu Phe Val Arg Asp Val | | | | |
| 210 | 215 | 220 | | |
| ctg ccg ggt gaa gcg att tat gtt acc ttt gat ggg caa tta cat tcg | 720 | | | |
| Leu Pro Gly Glu Ala Ile Tyr Val Thr Phe Asp Gly Gln Leu His Ser | | | | |
| 225 | 230 | 235 | 240 | |
| caa att tgt gcc gat aat cca aaa ctg aat cct tgt att ttt gaa tat | 768 | | | |
| Gln Ile Cys Ala Asp Asn Pro Lys Leu Asn Pro Cys Ile Phe Glu Tyr | | | | |
| 245 | 250 | 255 | | |
| gtt tat ttt gcc cgt cct gat tcc gtc att gat ggc gtt tct gta tat | 816 | | | |
| Val Tyr Phe Ala Arg Pro Asp Ser Val Ile Asp Gly Val Ser Val Tyr | | | | |
| 260 | 265 | 270 | | |
| tct gca cga gtg cat atg ggc gaa tta tta ggt gag aaa att aaa cgt | 864 | | | |
| Ser Ala Arg Val His Met Gly Glu Leu Leu Gly Glu Lys Ile Lys Arg | | | | |
| 275 | 280 | 285 | | |
| gaa tgg gga cga att atc gat gat att gat gtg gtg atc ccg att cct | 912 | | | |
| Glu Trp Gly Arg Ile Ile Asp Asp Ile Asp Val Val Ile Pro Ile Pro | | | | |
| 290 | 295 | 300 | | |
| gaa acc tca aat gat att gcg gta cgt att gct aat atg ttg tat aaa | 960 | | | |
| Glu Thr Ser Asn Asp Ile Ala Val Arg Ile Ala Asn Met Leu Tyr Lys | | | | |
| 305 | 310 | 315 | 320 | |
| ccc tat cgt caa ggg ttt gtt aaa aac cgc tat gta gct cga act ttt | 1008 | | | |
| Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Ala Arg Thr Phe | | | | |
| 325 | 330 | 335 | | |
| att atg ccg ggg caa gca cag cgt aaa agc tcg gtt cgc cgt aaa tta | 1056 | | | |
| Ile Met Pro Gly Gln Ala Gln Arg Lys Ser Ser Val Arg Arg Lys Leu | | | | |
| 340 | 345 | 350 | | |
| aat gcg att gcc tct gaa ttt aaa ggc aaa agc gtg tta ctg gtt gat | 1104 | | | |
| Asn Ala Ile Ala Ser Glu Phe Lys Gly Lys Ser Val Leu Leu Val Asp | | | | |
| 355 | 360 | 365 | | |
| gat tct att gta cga ggt aca acg tct gaa caa atc gtg gaa atg gca | 1152 | | | |
| Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala | | | | |
| 370 | 375 | 380 | | |
| cga gca gct ggt gca aaa cgg gtt tat ttt gcc tct gcc gca ccg gaa | 1200 | | | |
| Arg Ala Ala Gly Ala Lys Arg Val Tyr Phe Ala Ser Ala Ala Pro Glu | | | | |
| 385 | 390 | 395 | 400 | |

| | |
|---|------|
| att cgc tac ccg aat gtg tat ggc att gat atg ccg act tgt gaa gaa
Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Cys Glu Glu
405 410 415 | 1248 |
| tta gtg gct tat gat cgc tca gtg gaa gag gtt gca cag atg ata ggg
Leu Val Ala Tyr Asp Arg Ser Val Glu Glu Val Ala Gln Met Ile Gly
420 425 430 | 1296 |
| gtg gat aaa ttg att ttc caa gac ctt gaa gca ctt tat aag tct att
Val Asp Lys Leu Ile Phe Gln Asp Leu Glu Ala Leu Tyr Lys Ser Ile
435 440 445 | 1344 |
| caa ctg gaa aat ccg act att cat cgc ttt gat gac tct gta ttt aca
Gln Leu Glu Asn Pro Thr Ile His Arg Phe Asp Asp Ser Val Phe Thr
450 455 460 | 1392 |
| gga gaa tat att aca ggt gat gta gat aaa tgc tat tta gac agt ata
Gly Glu Tyr Ile Thr Gly Asp Val Asp Lys Cys Tyr Leu Asp Ser Ile
465 470 475 480 | 1440 |
| gca aga tct cga aac gat aaa gca aaa gca gag gcg gca aaa caa gcc
Ala Arg Ser Arg Asn Asp Lys Ala Lys Ala Glu Ala Ala Lys Gln Ala
485 490 495 | 1488 |
| acc aat tta gaa att cat aac gaa aga ta
Thr Asn Leu Glu Ile His Asn Glu Arg
500 505 | 1517 |
|
 | |
| <210> 173 | |
| <211> 505 | |
| <212> PRT | |
| <213> Pasteurella (Mannheimia) haemolytica | |
|
 | |
| <400> 173 | |
| Met Cys Gly Ile Val Gly Ile Ile Gly Asn Ser Pro Val Asn Gln Ala
1 5 10 15 | |
| Ile Tyr Asp Gly Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala
20 25 30 | |
| Gly Ile Val Thr Ile Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala
35 40 45 | |
| Asn Gly Leu Val Ser Asp Val Phe Gln Gln Glu His Met Val Arg Leu
50 55 60 | |
| Gln Gly Asn Val Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser
65 70 75 80 | |
| Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Phe Gly
85 90 95 | |
| Ile Thr Leu Val His Asn Gly Asn Leu Thr Asn Asn Ala Glu Leu Lys
100 105 110 | |
| Ala Arg Leu Tyr Asn Glu Ala Arg Arg His Val Asn Thr Asn Ser Asp
115 120 125 | |
| Ser Glu Ser Leu Leu Asn Ile Phe Ala Tyr Phe Leu Asp Leu Tyr Ser
130 135 140 | |

Thr Gln His Leu Ser Pro Asp Asn Ile Phe Glu Thr Val Arg Lys Thr
 145 150 155 160
 Asn Asp Ser Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly
 165 170 175
 His Gly Met Val Ala Phe Arg Asp Pro Phe Gly Ile Arg Pro Leu Val
 180 185 190
 Leu Gly Lys Arg Glu Ile Glu Gly Lys Thr Glu Tyr Met Phe Ala Ser
 195 200 205
 Glu Ser Val Ala Leu Asp Val Val Gly Phe Glu Phe Val Arg Asp Val
 210 215 220
 Leu Pro Gly Glu Ala Ile Tyr Val Thr Phe Asp Gly Gln Leu His Ser
 225 230 235 240
 Gln Ile Cys Ala Asp Asn Pro Lys Leu Asn Pro Cys Ile Phe Glu Tyr
 245 250 255
 Val Tyr Phe Ala Arg Pro Asp Ser Val Ile Asp Gly Val Ser Val Tyr
 260 265 270
 Ser Ala Arg Val His Met Gly Glu Leu Leu Gly Glu Lys Ile Lys Arg
 275 280 285
 Glu Trp Gly Arg Ile Ile Asp Asp Ile Asp Val Val Ile Pro Ile Pro
 290 295 300
 Glu Thr Ser Asn Asp Ile Ala Val Arg Ile Ala Asn Met Leu Tyr Lys
 305 310 315 320
 Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Ala Arg Thr Phe
 325 330 335
 Ile Met Pro Gly Gln Ala Gln Arg Lys Ser Ser Val Arg Arg Lys Leu
 340 345 350
 Asn Ala Ile Ala Ser Glu Phe Lys Gly Lys Ser Val Leu Leu Val Asp
 355 360 365
 Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala
 370 375 380
 Arg Ala Ala Gly Ala Lys Arg Val Tyr Phe Ala Ser Ala Ala Pro Glu
 385 390 395 400
 Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Cys Glu Glu
 405 410 415
 Leu Val Ala Tyr Asp Arg Ser Val Glu Glu Val Ala Gln Met Ile Gly
 420 425 430
 Val Asp Lys Leu Ile Phe Gln Asp Leu Glu Ala Leu Tyr Lys Ser Ile
 435 440 445
 Gln Leu Glu Asn Pro Thr Ile His Arg Phe Asp Asp Ser Val Phe Thr
 450 455 460
 Gly Glu Tyr Ile Thr Gly Asp Val Asp Lys Cys Tyr Leu Asp Ser Ile
 465 470 475 480

Ala Arg Ser Arg Asn Asp Lys Ala Lys Ala Glu Ala Ala Lys Gln Ala
 485 490 495

Thr Asn Leu Glu Ile His Asn Glu Arg
 500 505

<210> 174
 <211> 386
 <212> DNA
 <213> Pasteurella (Mannheimia) haemolytica

<220>
 <221> CDS
 <222> (1)..(384)

<220>
 <223> yjgF

<400> 174
 atg aca gtt atc cac aca gaa aat gca ccg gca gcg att ggg cct tat 48
 Met Thr Val Ile His Thr Glu Asn Ala Pro Ala Ala Ile Gly Pro Tyr
 1 5 10 15

gtg caa gca gtt gat tta ggc aat atg gtt tta act tct ggg caa att 96
 Val Gln Ala Val Asp Leu Gly Asn Met Val Leu Thr Ser Gly Gln Ile
 20 25 30

ccc gtg aat cct gaa acc ggc gaa atc ccg agt gat att gtg caa caa 144
 Pro Val Asn Pro Glu Thr Gly Glu Ile Pro Ser Asp Ile Val Gln Gln
 35 40 45

acc cgc caa tct ctg aac aac gtg aaa gcc att atc gaa caa gcc ggc 192
 Thr Arg Gln Ser Leu Asn Asn Val Lys Ala Ile Ile Glu Gln Ala Gly
 50 55 60

tta acc gtt gcc gat att gta aag acc acc gta ttt gtc aaa gat ctt 240
 Leu Thr Val Ala Asp Ile Val Lys Thr Thr Val Phe Val Lys Asp Leu
 65 70 75 80

aac gac ttc gca aag gta aat gcg gaa tac caa gcc ttc ttc caa gaa 288
 Asn Asp Phe Ala Lys Val Asn Ala Glu Tyr Gln Ala Phe Phe Gln Glu
 85 90 95

aac gaa cac cct aat ttt ccg gct cgt tct tgc gta gaa gtg gct cgt 336
 Asn Glu His Pro Asn Phe Pro Ala Arg Ser Cys Val Glu Val Ala Arg
 100 105 110

tta cca aaa gat gtt ggc att gag atc gaa gcg att gca gta cgc cga 384
 Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala Val Arg Arg
 115 120 125

ta 386

<210> 175
 <211> 128
 <212> PRT
 <213> Pasteurella (Mannheimia) haemolytica

<400> 175
 Met Thr Val Ile His Thr Glu Asn Ala Pro Ala Ala Ile Gly Pro Tyr
 1 5 10 15

Val Gln Ala Val Asp Leu Gly Asn Met Val Leu Thr Ser Gly Gln Ile
20 25 30

Pro Val Asn Pro Glu Thr Gly Glu Ile Pro Ser Asp Ile Val Gln Gln
35 40 45

Thr Arg Gln Ser Leu Asn Asn Val Lys Ala Ile Ile Glu Gln Ala Gly
50 55 60

Leu Thr Val Ala Asp Ile Val Lys Thr Thr Val Phe Val Lys Asp Leu
65 70 75 80

Asn Asp Phe Ala Lys Val Asn Ala Glu Tyr Gln Ala Phe Phe Gln Glu
85 90 95

Asn Glu His Pro Asn Phe Pro Ala Arg Ser Cys Val Glu Val Ala Arg
100 105 110

Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala Val Arg Arg
115 120 125

<210> 176
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<221>
<222>
<223> Description of Artificial Sequence: PRIMER

<400> 176
atggcnggng cnaargarat 20

<210> 177
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<221>
<222>
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<220>
<221> misc_feature
<222> 3
<223> n = A or T or G or C

<220>
<221> misc_feature
<222> 12
<223> n = A or T or G or C

<220>
<221> misc_feature
<222> 15
<223> n = A or T or G or C

<400> 177
gcngcyttca tngcnaccat 20

<210> 178

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<220>
<221> misc_feature
<222> 3
<223> N = A or T or G or C

<400> 178
ggnttyatyc ayaaaaayat g

21

<210> 179
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<220>
<221> misc_feature
<222> 6
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 12
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 15
<223> N = A or T or G or C

<400> 179
tcttngtra tngtnacatc rtg

23

<210> 180
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 180
gcsggyaaac crcgttggga ttgg

24

<210> 181
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 181
crcctaarat rtctgaaagc accac

25

<210> 182
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<220>
<221> misc_feature
<222> 9
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 15
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 18
<223> N = A or T or G or C

<400> 182

atgtgyggna tygtnggnat 20

<210> 183
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 183
catatatcaata ccatacacat t 21

<210> 184
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<220>
<221> misc_feature
<222> 3
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 6
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 12
<223> N = A or T or G or C

<400> 184
ggncctayg tncarg 16

<210> 185
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<220>
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<222> 1
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 4
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 10
<223> N = A or T or G or C

<400> 185
ngcnacytcn acrca 15

<210> 186
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 186
gaagccgcca tacgctcttg gg 22

<210> 187
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 187
gttgcttcct ttgcctgcac tgg 23

<210> 188
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 188
ggctcagaaa caataccact ttca 24

<210> 189
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 189
gcaccaaaggc agaatttgc c 21

<210> 190
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 190
ggtgatgtatg tcgatgatag tccc 24

<210> 191
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 191
ggcgtagatcc ccgtgtgcc aacc 24

<210> 192
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 192
gaccacttag gcgatatgga ctt 23

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<220>
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<220>
<223> Description of Artificial Sequence: PRIMER

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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: PRIMER

<400> 195
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<210> 196
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 196
cgcccggttc aggattcacg gg 22

<210> 197
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 197
ctgaacaacg tgaaagccat 20

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09/809,665 15 March 2001 (15.03.2001) US

(71) Applicant (for all designated States except US): **PHARMACIA & UPJOHN COMPANY [US/US]**; 301 Henrietta Street, Kalamazoo, MI 49007 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **LOWERY, David, E.** [US/US]; 1207 Woodland Drive, Portage, MI 49024 (US). **FULLER, Troy, E.** [US/US]; 111 Dreamfield Drive, Battle Creek, MI 49014 (US). **KENNEDY, Michael, J.** [US/US]; 2364 Quincy Avenue, Portage, MI 49024 (US).

(74) Agent: **WILLIAMS, Joseph, A., Jr.**; Marshall, Gerstein & Borun, 6300 Sears Tower, 233 South Wacker Drive, Chicago, IL 60606 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

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For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

WO 02/075507 A3

(54) Title: ANTI-BACTERIAL VACCINE COMPOSITIONS

(57) Abstract: Gram negative bacterial virulence genes are identified, thereby allowing the identification of anti-bacterial agents that target these virulence genes and their products, and the provision of gram negative bacterial mutants useful in vaccines.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 02/01971

A. CLASSIFICATION OF SUBJECT MATTER

| | | | | | |
|-------|------------|------------|-----------|-----------|-----------|
| IPC 7 | C12N1/20 | A61K39/102 | A61K35/74 | C12N15/31 | C12N15/63 |
| | C07K14/285 | C07K16/12 | C12Q1/18 | G01N33/68 | |

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N A61K C07K C12Q G01N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EMBL, EPO-Internal, WPI Data, BIOSIS, MEDLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

| Category ^o | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|-----------------------|---|-----------------------|
| X | DATABASE EMBL [Online]
10 February 2001 (2001-02-10)
MAY B.J. ET AL.: "Pasteurella multocida
PM70 section 152 of 204 of the complete
genome"
Database accession no. AE006064
XP002224305
nucleotides 3352-4146
& DATABASE EMBL [Online]
Entry AE006064,
10 February 2001 (2001-02-10)
MAY B.J. ET AL.: "Pasteurella multocida
PM70 section 31 of 204 of the complete
genome"
the whole document | 1-41 |
| X | & BARBARA J. MAY ET AL.: "Complete
genomic sequence of Pasteurella multocida,
PM70"
PROCEEDINGS OF THE NATIONAL ACADEMY OF
-/- | 5-23, 25,
28 |
| A | | 1-41 |

 Further documents are listed in the continuation of box C. Patent family members are listed in annex.

° Special categories of cited documents :

- "A" document defining the general state of the art which is not considered to be of particular relevance
- "E" earlier document but published on or after the international filing date
- "L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- "O" document referring to an oral disclosure, use, exhibition or other means
- "P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

12 May 2003

Date of mailing of the international search report

16. 05. 2003

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL-2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl.
Fax: (+31-70) 340-3016

Authorized officer

Montero Lopez, B

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 02/01971

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

| Category ° | Citation of document, with indication, where appropriate, of the relevant passages | Relevant to claim No. |
|------------|--|-----------------------|
| X | <p>SCIENCES OF USA,
vol. 98, no. 6,
13 March 2001 (2001-03-13), pages
3460-3465, XP002202785
WASHINGTON US
page 3463, right-hand column, paragraph 2
-page 3464, left-hand column, paragraph 1</p> <p>---</p> <p>COONEY ET AL: "Three contiguous
lipoprotein genes in <i>Pasteurella</i>
<i>haemolytica</i> A1 which are homologous to a
lipoprotein gene in <i>Haemophilus influenza</i>
Type b"</p> <p>INFECTION AND IMMUNITY, AMERICAN SOCIETY
OF MICROBIOLOGY, WASHINGTON, DC, US,
vol. 61, no. 11, November 1993 (1993-11),
pages 4682-4688, XP002148894
ISSN: 0019-9567
abstract
page 4683, left-hand column, last
paragraph -page 4685, left-hand column,
paragraph 1; figures 3,4
page 4686, right-hand column, paragraph 2</p> <p>---</p> | 5-23,25,
28 |
| A | <p>TROY E. FULLER ET AL.: "Identification of
<i>Pasteurella multocida</i> virulence genes in a
septicemic mouse model using
signature-tagged mutagenesis"</p> <p>MICROBIAL PATHOGENESIS,
vol. 29, 2000, pages 25-38, XP002224304
the whole document</p> <p>-----</p> | 1-41 |

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US 02/01971

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. Claims Nos.: because they relate to subject matter not required to be searched by this Authority, namely:

2. Claims Nos.: because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. Claims Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
1-41 partially

4. No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- The additional search fees were accompanied by the applicant's protest.
- No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-41 partially

Gram-negative bacteria comprising a mutation in a gene of sequence SEQ ID NO:1 resulting in decreased activity of the gene product; immunogenic composition comprising the bacteria; method of producing such mutant bacteria; nucleotide sequence comprising SEQ ID NO:1, vector and host cell comprising the same and use thereof to produce a polypeptide; encoded polypeptide of sequence SEQ ID NO:2; antibody against it; use of the polypeptide of sequence SEQ ID NO:2 for identifying antibacterial agents.

2. Claims: 1-41 partially

Idem as subject 1 for, respectively sequences SEQ ID NO:3 and 4; 7 and 8; 9 and 10; 21 and 22; 25 and 26.

3. Claims: 1-4, 21-23, 27, 28 partially

Gram-negative bacteria comprising a mutation in a gene of sequence SEQ ID NO:27 resulting in decreased activity of the gene product; immunogenic composition comprising the bacteria; nucleotide sequence comprising SEQ ID NO:27.

4. Claims: 1-41 partially

Idem as subject 1 for, respectively, sequences SEQ ID NOS:29 and 30; 39 and 40; 41 and 42; 51 and 52; 53 and 54; 55 and 56.

5. Claims: 1-28 partially

Gram-negative bacteria comprising a mutation in a gene of sequence SEQ ID NO:57 resulting in decreased activity of the gene product; immunogenic composition comprising the bacteria; method of producing such mutant bacteria; nucleotide sequence comprising SEQ ID NO:57.

6. Claims: 1-41 partially

Idem as subject 1 for, respectively sequences SEQ ID NOS:58 and 59; 60 and 61; 68 and 69; 72 and 73; 74 and 75; 76 and 77; 78 and 79; 80 and 81; 82 and 83; 84 and 85; 104 and 105; 108 and 109; 112 and 113; 116 and 117; 118 and 119; 120 and 121; 122 and 123; 124 and 125; 126 and 127; 128 and 129; 130 and 131

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

7. Claims: 5-26, 29-41 partially

Attenuated Pasteurellaceae bacteria comprising a mutation in a gene of sequence SEQ ID NO:11; immunogenic composition containing it; method of producing such mutant bacteria; nucleotide sequence comprising SEQ ID NO:11, vector and host cell comprising the same and use thereof to produce a polypeptide; encoded polypeptide of sequence SEQ ID NO:12; antibody against it; use of the polypeptide of sequence SEQ ID NO:12 for identifying antibacterial agents.

8. Claims: 5-26, 28-41 partially

Idem as subject 36 for, respectively, sequences SEQ ID NOs:13 and 14; 15 and 16; 17 and 18; 19 and 20; 23 and 24; 31 and 32; 33 and 34; 35 and 36; 37 and 38; 70 and 71; 100 and 101; 102 and 103; 106 and 107; 110 and 111; 114 and 115; 132 and 133; 134 and 135; 136 and 137; 138 and 139; 140 and 141; 142 and 143; 144 and 145; 146 and 147; 148 and 149; 150 and 151; 152 and 153; 154 and 155; 156 and 157; 158 and 159; 160 and 161

9. Claims: 5-26 partially

Attenuated Pasteurellaceae bacteria comprising a mutation in, respectively a gene of sequence SEQ ID NO:162 and 163; immunogenic composition containing it; method of producing such mutant bacteria; nucleotide sequence comprising SEQ ID NO:162 or 163.

10. Claims: 5-26, 28-41 partially

Idem as subject 36 for, respectively, sequences SEQ ID NOs:164 and 165; 166 and 167; 168 and 169; 170 and 171; 172 and 173; 174 and 175

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(10) International Publication Number
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A61K 39/102, 35/74, C12N 15/31, 15/63, C07K 14/285,
16/12, C12Q 1/18, G01N 33/68

(21) International Application Number: PCT/US02/01971

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(25) Filing Language: English

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(30) Priority Data:
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(71) Applicant (for all designated States except US): **PHARMACIA & UPJOHN COMPANY [US/US]**; 301 Hemmetta Street, Kalamazoo, MI 49007 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **LOWERY, David, E.** [US/US]; 1207 Woodland Drive, Portage, MI 49024 (US). **FULLER, Troy, E.** [US/US]; 111 Dreamfield Drive, Battle Creek, MI 49014 (US). **KENNEDY, Michael, J.** [US/US]; 2364 Quincy Avenue, Portage, MI 49024 (US).

(74) Agent: **WILLIAMS, Joseph, A., Jr.**; Marshall, Gerstein & Borun, 6300 Sears Tower, 233 South Wacker Drive, Chicago, IL 60606 (US).

(81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CI, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GII, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

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- with amended claims

(88) Date of publication of the international search report:
12 September 2003

Date of publication of the amended claims: 11 December 2003

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.



WO 02/075507 A3

(54) Title: ANTI BACTERIAL VACCINE COMPOSITIONS

(57) Abstract: Gram negative bacterial virulence genes are identified, thereby allowing the identification of anti-bacterial agents that target these virulence genes and their products, and the provision of gram negative bacterial mutants useful in vaccines.

AMENDED CLAIMS

[received by the International Bureau on 11 July 2003 (11.07.03)
original claims 1 to 41 have been amended by claims 1 to 29

WHAT IS CLAIMED IS:

1. An attenuated *Mannheimia* bacteria comprising a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOS: 166, 168, 170, 172 and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.
5
2. The *Mannheimia* bacteria of claim 1 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.
- 10 3. The *Mannheimia* bacteria of claim 1 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.
4. The *Mannheimia* bacteria of claim 1 wherein said mutation results in deletion of all or part of said gene.
15
5. The *Mannheimia* bacteria of claim 1 wherein the *Mannheimia bacteria* is *Mannheimia haemolytica*.
6. The *Mannheimia* bacteria of claim 5 wherein said mutation results in
20 decreased expression of a gene product encoded by the mutated gene.
7. The *Mannheimia* bacteria of claim 5 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.
- 25 8. The *Mannheimia* bacteria of claim 5 wherein said mutation results in deletion of all or part of said gene.
9. An immunogenic composition comprising the bacteria according to
any one of claims 1 through 8.
30

10. A vaccine composition comprising the immunogenic composition according to claim 9 and a pharmaceutically acceptable carrier.

11. The vaccine composition according to claim 10 further comprising an
5 adjuvant.

12. A method for producing a gram-negative bacteria mutant comprising the step of introducing a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOS: 166, 168, 170, 172, and 174 or a species homolog
10 thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

13. A method for producing an attenuated *Mannheimia* bacteria comprising the step of introducing a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOS: 166, 168, 170, 172, and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.
15

14. A purified and isolated *Mannheimia* polynucleotide comprising a
20 nucleotide sequence selected from the group consisting of nucleotide sequences set forth in SEQ ID NOS: 166, 168, 170, 172 and 174.

15. A purified and isolated *Mannheimia* polynucleotide comprising a nucleotide sequence as set forth in SEQ ID NO: 166.
25

16. A purified and isolated polynucleotide encoding a *Mannheimia* virulence gene product, or species homolog thereof, selected from the group consisting of:

- a) the polynucleotide according to claim 14;

- b) polynucleotides encoding a polypeptide encoded by the polynucleotide of (a); and
- c) polynucleotides that hybridize to the complement of the polynucleotides of (a) or (b) under moderate stringency conditions.

5

17. A purified and isolated *Mannheimia* polynucleotide encoding a polypeptide selected from the group consisting of polypeptides having amino acid sequences set forth in SEQ ID NOS: 167, 169, 171, 173, and 175.

10

18. The polynucleotide of claim 17 which is a DNA.

19. A vector comprising the DNA of claim 18.

20. The vector of claim 19 that is an expression vector, wherein the DNA
15 is operatively linked to an expression control DNA sequence.

21. A host cell stably transformed or transfected with the DNA of claim 18
in a manner allowing the expression of the encoded polypeptide in said host cell.

20

22. A method for producing a recombinant polypeptide comprising
culturing the host cell of claim 21 in a nutrient medium and isolating the encoded
polypeptide from said host cell or said nutrient medium.

23. A purified polypeptide produced by the method of claim 22.

25

24. A purified polypeptide comprising a polypeptide selected from the
group consisting of polypeptides having amino acid sequences set forth in SEQ ID
NOS: 167, 169, 171, 173, and 175.

25. An antibody that is specifically reactive with the polypeptide of claim
24.

26. The antibody of claim 25 that is a monoclonal antibody.

5

27. A method of using the monoclonal antibody of claim 26 for identifying
a bacteria of claims 1 or 5, comprising the steps of contacting an extract of bacteria
with said monoclonal antibody and detecting the absence of binding of said
monoclonal antibody.

10

28. A method of identifying an anti-bacterial agent comprising the steps of
assaying potential agents for the ability to interfere with expression or activity of gene
products represented by the amino acid sequences set forth in any one of SEQ ID
NOS: 167, 169, 171, 173, and 175 and identifying an agent that interferes with
15 expression or activity of said gene products.

29. A method of identifying an anti-bacterial agent comprising the steps
of:

- a) measuring expression or activity of a gene product as set out in
20 any one of SEQ ID NOS: 167, 169, 171, 173, and 175;
- b) contacting the gene product in (a) with a test compound;
- c) measuring expression or activity of the gene product in the
presence of the test compound; and
- d) identifying the test compound as an antibacterial agent when
25 expression or activity of the gene product is decreased in the presence of the test
compound as compared to expression or activity in the absence of the test compound.